

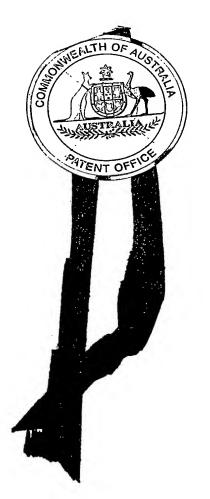
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I, LEANNE MYNOTT, MANAGER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. 2003901796 for a patent by AGRICULTURE VICTORIA SERVICES PTY LTD and AGRESEARCH LIMITED as filed on 14 April 2003.



WITNESS my hand this Twenty-eighth day of April 2004

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AUSTRALIA
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Patents Act 1990

## PROVISIONAL SPECIFICATION

Invention Title: Manipulation of organic acid biosynthesis and secretion

The invention is described in the following statement:

### MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid metabolism (CAM) photosynthesis, stomatal and pulvinual movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation Al<sup>3+</sup> which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors NAD<sup>+</sup> and FAD, forming NADH, FADH<sub>2</sub>, and carbon dioxide (CO<sub>2</sub>). The reaction sequence of the TCA cycle involves: in a reaction catalyzed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C<sub>6</sub> tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of CO<sub>2</sub> in a series of reactions that leads to the formation of one oxaloacetate, three NADH, one FADH<sub>2</sub>, and one ATP. The resulting oxaloacetate reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional CO<sub>2</sub> and NADH. Thus the TCA cycle brings about the complete oxidation of pyruvate to three CO<sub>2</sub> plus 10 electrons, which are stored temporarily as 4 NADH and 1 FADH<sub>2</sub>.

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Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form CO<sub>2</sub>, acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well as free coenzyme A (CoASH) and NAD<sup>+</sup>, links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate carboxylase.

In particular, citrate synthase (CS) catalyzes the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyzes the final step of the TCA cycle, oxidizing malate to oxaloacetate and producing NADH. This reaction catalyzed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an NADP+-dependent MDH that plays a critical role in balancing reducing equivalents between the cytosol and stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in β-oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and

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alfalfa ( $Medicago\ sativa$ ), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of  $N_2$  by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyzes the reaction of phosphoenol-pyruvate with HCO<sub>3</sub> releasing the phosphate and producing the C4 product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malata dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO<sub>2</sub> fixation in C<sub>4</sub> and Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorous acquisition efficiency in plants; in modifying aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic enzymes CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species which are related to CS, MDH and PEPC, or functionally active fragments or variants thereof. Such proteins are referred to herein as CS-like, MDH-like and PEPC-like respectively.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene

activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses,

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respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

The term "purified" means that the nucleic acid or polypeptide is substantially free of other nucleic acids or polypeptides.

By "functionally active" in respect of a nucleotide sequence it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

By "functionally active" in the context of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino 5 acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

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By "operatively linked" in respect of a regulatory element, nucleic acid or nucleic acid fragment and terminator, it meant that the regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

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Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an CS or CS-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (b) complements of the sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MDH or MDH-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (b) complements of the sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an PEPC or PEPC-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86,

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88, 89, 91, 92, 94, 95 and 97 hereto; (b) complements of the sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific 10 oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available in vitro transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman et al. (1988) Proc. Natl. Acad Sci. USA 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara et al. (1989) Proc. Natl. Acad Sci USA 86:5673; Loh et al. (1989) Science 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (Trifolium), medic (Medicago), ryegrass (Lolium) or fescue (Festuca) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins; and functionally active fragments and variants thereof.

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The clover (Trifolium), medic (Medicago), ryegrass (Lolium) or fescue (Festuca) species may be of any suitable type, including white clover (Trifolium repens), red clover (Trifolium pratense), subterranean clover (Trifolium subterraneum), alfalfa (Medicago sativa), Italian or annual ryegrass (Lolium multiflorum), perennial ryegrass (Lolium perenne), tall fescue (Festuca arundinacea), meadow fescue (Festuca pratensis) and red fescue (Festuca rubra). 15 Preferably the species is a clover or a ryegrass, more preferably white clover (T. repens) or perennial ryegrass (L. perenne).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 10, 185 and 188 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown 30 in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96 and 98 hereto, and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

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Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 79, 89, 92, 104, 122, 131, 142, 145, 148, 151, 154, 157, 163, 173, 179, 186, 189, 192, 200, 203, 209, 226, 232, 246, 255 and 262 hereto.

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Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 66, 67, 72, 78, 88, 94, 101and 104 hereto; or complements or sequences antisense thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence

information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic acid soils; in relation to nutrient acquisition efficiency including phosphorus; in relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a vector including a nucleic acid or nucleic acid fragment according to the present invention.

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In a preferred embodiment of this aspect of the invention, the vector may include a regulatory element such as a promoter, a nucleic acid or nucleic acid fragment according to the present invention and a terminator; said regulatory element, nucleic acid or nucleic acid fragment and terminator being operatively linked.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, nonchromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from Agrobacterium tumefaciens, derivatives of the Ri plasmid from Agrobacterium rhizogenes; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids 25 and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue specific promoters include root prevalent promoters.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (nos) and the octopine synthase (ocs) genes.

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The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such

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techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera Lolium, 5 Festuca, Paspalum, Pennisetum, Panicum and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (Lolium species) and fescues (Festuca species), more preferably perennial ryegrass, including . forage- and turf-type cultivars. In an alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (Trifolium species) and medics (Medicago species), more preferably white clover (Trifolium repens), red clover (Trifolium pratense), subterranean clover (Trifolium subterraneum) and alfalfa (Medicago sativa). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include Agrobacterium mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be . transformed.

Cells incorporating the vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (Lolium species) or fescue (Festuca species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (Trifolium species) and medics (Medicago species), more preferably white clover (Trifolium repens), red clover (Trifolium pratense), subterranean clover (Trifolium subterraneum) and alfalfa (Medicago sativa).

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The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying organic acid biosynthesis; of modifying organic acid secretion; of modifying phosphorous and other nutrients acquisition efficiency in plants; of modifying aluminium and acid soil tolerance in plants; of modifying nitrogen fixation and nodule function, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to the present invention. Preferably the nucleic acid or nucleic acid fragment is part of a vector.

Using the methods and products of the present invention, organic acid biosynthesis; organic acid secretion; phosphorous and other plant nutrient acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and nodule function, may be increased or otherwise altered, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise altered, for example

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by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

10 Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSd.

Figure 10 shows the deduced amino acid sequence of LpCSd.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb.

Figure 15 shows the deduced amino acid sequence of LpMDHb.

Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc.

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

Figure 21 shows the nucleotide sequence of LpMDHe.

5 Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

10 Figure 26 shows the nucleotide sequence of LpMDHg.

Figure 27 shows the deduced amino acid sequence of LpMDHg.

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

Figure 31 shows the nucleotide sequence of LpMDHi.

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

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Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHI.

25 Figure 39 shows the deduced amino acid sequence of LpMDHI.

Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

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Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

25 Figure 62 shows the deduced amino acid sequence of TrMDHc.

Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

5 Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj.

Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa.

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

5 Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

10 Figure 93 shows the deduced amino acid sequence of TrPEPCc.

Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc.

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

15 Figure 97 shows the nucleotide sequence of TrPEPCe.

Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

#### EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

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cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

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TABLE 1 cDNA libraries from white clover (Trifolium repens)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 &28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated wc
04wc	Nodulated wc cut leaf and stem collected after 0, 1, 4, 6 &14 h after cutting
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at -80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials

0	75
7	, and a
<b>V</b>	

Library		Organ/Tissue	
15wc	Senescing stolon		· · · · · · · · · · · · · · · · · · ·
16wc	Senescing leaf		

TABLE 2 cDNA libraries from perennial ryegrass (Lolium perenne)

Library	Organ/Tissue							
01rg	Roots from 3-4 day old light-grown seedlings							
02rg	Leaves from 3-4 day old light-grown seedlings							
03rg	Etiolated 3-4 day old dark-grown seedlings							
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)							
05rg	Senescing leaves from mature plants							
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)							
07rg	Roots from mature plants grown in hydroponic culture							
08rg	Senescent leaf tissue							
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)							
10rg	Embryogenic suspension-cultured cells							
11rg	Non-embryogenic suspension-cultured cells							
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)							
13rg	Shoot apices including vegetative apical meristems							
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development							

Library	Organ/Tissue
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (rbcL, rbcS, cab, wir2A subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts)  (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into Escherichia coli Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

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Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into E. coli DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit 15 (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

#### **EXAMPLE 2**

#### DNA sequence analyses

The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-

like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul et al. (1993) J. Mol. Biol. 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) Nature Genetics 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to

a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

10 Agriculture Victoria Services Pty Ltd

and

**AgResearch Limited** 

By their Registered Patent Attorneys

Freehills Carter Smith Beadle

14 April 2003

			*	20	*	40	* አጸጥጥር አርርስ	60 GGT :		60
LpCSa	:	GNNTTATAT	TGACGGGG	ATGAGGGAATT	CTTCGCTAC	AGAGGCTATCC	AAT TGAGGA		•	
			*	80	*	100	*	120		100
LpCSa	<b>:</b>	GGCTGAAAG	CAGCTCGT	TTGTTGAGGTC	GCCTACCTC	TTAATGTATGG	GAATTTGCC	CAC	:	120
			*	140	*	160	* .	180		
LpCSa	:	CCAGAGTCA	ACTGGCAG	GCTGGGAGTTT	GCAATTTCC	3CAGCACTCTGC	TGTTCCTC	AAGG	:	180
				200	*	220 .	*	240		
LpCSa	:	ACTCTTGGA	TATAATAC	AATCAATGCCT	CATGATGC	CACCCATGGG	TGTCCTTG	CCAG	:	240
						222		300		
LpCSa	:	TGCAATGAG	* CACACTTT	260 CAGTCTTCCAT	* CCAGATGC	280 AAACCCTGCTCI	TAGAGGTC		:	300
LpCSa	:	TCTATACAA	* GTCGAAGO	320 AGGTTAGGGAT	* · 'AAGCAAAT'	340 TGTACGAGTTCI	* TGGGAAGG	360 CACC	:	360
T = CCc	_	አረመእ አሞአርረ	* ************************************	380 . ברכיימירטיקמקמ	* TTAGCAGG	400 Aaggccctttg:	* rccttcctt	420 CAAA	:	420
прсза	•	AGIANIAG	Accidenc							
			*	440	*	460	* ************************************	480		480
LpCSa	:	TAATCTCTC	CTTATTCAG	SAAAATTTCTTG	TATATGCT	GGACTCTATGG(	JIGACAAAG		•	100
			*	500	*	520	*	540		<b>540</b>
LpCSa	:	TAAGCCAA	ATCCCAGAC	CTTGCCCGGGTI	CTGGATGT	CCTTTTTATTC'	rtcatgcig	AACA	:	540
			*	560	*	580	*	600		
LpCSa	:	CGAAATGA	ACTGCTCAF	ACAGCTGCTGTT	PAGGCACCT	TGCTTCAAGTG	<b>3TGTCGATG</b>	TCTT	:	600
		ŧ	*	620	*	640	*	660		
LpCSa	:	CACTGCTC	TTTCTGGT	CTGTTGGAGCT	CTATATGG	TCCACTGCATG	GTGGCGCAA	ATGA	:	660
			*	680	*	700	*	720		
LpCSa	:	GGCGGTAC	TTAAAATG:	TTAAATGAGATT	rggaagtgt	AGAGAATATTC	CGGAATTCA	TTGA	:	720
				540		760	· *	780		
LpCSa	:	GGGAGTGA	* AGAACAGGI	740 AAGCGGAAAATC	GTCTGGTTI	TGGGCACCGTG	TGTATAAGA		:	780
LpCSa	:	TGATCCTC	* GTGCTAAA	800 GTCATCCGGAA	* GTTAGCGG#	820 AGGAGGTTTTCA	* CGATTGTGG	840 GACG	:	840
-										
Tadas		CCATCCTC	* ጥጥ <u>አጥ</u> ፖርጳአር፥	860 GTAGCTGTTGC	* TTTGGAGA	880 AGGCAGCACTGT	* CAGACGAGT	000 TTTA1	:	900
npcsa	•	GGMICCIC	TIMICONG							
<b>.</b>			*	920	*	940 \TTCTGGCCTA	* ጥልጥልጥልናናርሳ	960 CAAT		960

\* . 1000 LpCsa : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCCAACAGGT : 1080 ·1100 LpCsa : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 1140 LpCsa : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGCTC : 1200 LPCSa : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 1260 LpCsa : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 1380 LPCSa : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 1440 LpCsa : TATCTTGAAAGTCTTAATCATGTGGACCAATGAAGACATAGATCAAGTTCTTTGCATGGG : 1500 

LpCSa : CGGCGGCTGTTTCTTTGGGAAAAAACTTTTTATGGGAGTCTTTTTTACC : 1550

		*	2	:0	k	40	k	60	
LpCSa	:	YIDGDEGILR	YRGYPIEEV	AESSSFVEVA	YLLMYGNL	PTQSQLAGWEFA:	ISQHSAVP	QGL :	60
LpCSa	, •	* TIDITTOSMPHO		0 SAMSTLSVFHPI		100 QDLYKSKQVRDK		120 APV :	120
2000	•						-		
LpCSa	:	* IAAAAYLRLA	14 GRPFVLPSN			160 DYKPNPRLARVL		180 EHE :	180
		·_			•	220		240	
LpCSa	:	MNCSTAAVRH	LASSGVDVE			NEAVLKMLNEIG			240
		*	26			280	*	300	300
LpCSa	:	VKNRKRKMSG	FGHRVYKN	DPRAKVIRKL	AEEVFTIV	GRDPLIEVAVAL	EKAALSDE	XFI :	300
LpCSa	:	* KRKLYPNVDF	32 YSGLIYRAN			340 WLAHWKESLDDP	* DNKIMRPÇ	360 QVY :	360
			. 38	20		400			
LpCSa	:	TGTWLRHYTE	•	SU DSEQLGQIATS					

Figure 3 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSa

		* 20 * 40 * 60		
		20		60
LpCSal	:	GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT		-
LpCSa2	:			_
LpCSa3	:			-
LpCSa4	:		:	-
LpCSa5	:		:	-
LpCSa6	:		:	-
LpCSa7	:		:	-
LpCSa8	:		:	-
		* 80 * 100 · * <u>120</u>		
LpCSa1	:	GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC	:	120
LpCSa2			:	-
LpCSa3			:	-
LpCSa4	:		:	-
LpCSa5	:		:	-
LpCSa6	:		:	-
LpCSa6	•		:	-
	•		:	-
LpCSa8	•			
		* 140 * 160 * 180		
T00-3		CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG	:	180
LpCSal	•	CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCA-CACTCTGCTGTTCCTCANGN	:	46
LpCSa2	:	GCAGGCIGGGAGIIIGCAAIIICGCA	:	_
LpCSa3	:		:	_
LpCSa4	:		:	_
LpCSa5	:		:	_
LpCSa6	:		•	_
LpCSa7	:		:	_
LpCSa8	:		•	-
		* 200 * 220 * 240		
		* 200 * 220 * 240 ACTCTTGGATATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG		240
LpCSa1	:	ACTCTTGGATATACTACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAGACCCCATGGGTGTCCTTGCCAG		106
LpCSa2	:	ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGGGTG	,	-
LpCSa3	:		•	_
LpCSa4	:			_
LpCSa5	:		:	_
LpCSa6	:		•	_
LpCSa7	:		:	_
LpCSa8	:		•	
		* 260 * 280 * 300		
				300
LpCSa1		TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA	:	166
LpCSa2		TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA		T00
LpCSa3			•	_
LpCSa4			•	_
LpCSa5			:	-
LpCSa6	:		:	-
LpCSa7	:		:	-
LpCSa8			:	-

Tu 0000	* 320 * 340 * 360  TCTATACAGTCGAGCAGGTTAGGGATAGCAAATTGTACGAGTTCTTGGGAAGGCACC	: 360
LpCSa1 :	TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC	: 226
LpCSa2 :	TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCAGC	. 220
LpCSa3 : LpCSa4 :		· : -
LpCSa5:		: -
LpCSa6:		: -
LpCSa7:	##************************************	: -
LpCSa8 :	***************************************	: -
<b></b>		
-	* 380 * 400 * 420	
LpCSa1 :	$\mathtt{AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCC}$ $\mathtt{TTTGTCCTTCCAAA}$	: 420
LpCSa2 :	AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCAAA	: 286
LpCSa3 :		: -
LpCSa4 :		: -
LpCSa5 :		: -
LpCSa6 :		: -
LpCSa7 :		: -
LpCSa8 :	·	: -
	* 440 * 460 * 480	
LpCSal :	TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA	: 480
LpCSa2 :	TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA	: 346
LpCSa3 :		: -
LpCSa4 :		: -
LpCSa5 :		: -
LpCSa6 :		
LpCSa7 : LpCSa8 :		· • -
презав :	•	•
	* 500 * 520 * 540	
LpCSal :	TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA	: 540
LpCSa2 :	TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA	
LpCSa3 :		: 406
T C C 4	TINTGCTG-ACA	: 406 : 12
LpCSa4 :		
LpCSa5 :		
LpCSa5 : LpCSa6 :		
LpCSa5 : LpCSa6 : LpCSa7 :		
LpCSa5 : LpCSa6 :		
LpCSa5 : LpCSa6 : LpCSa7 :		
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 :	* 560 * 580 * 600	: 12 : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 : LpCSa1 : LpCSa2 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCsa5 : LpCsa6 : LpCsa7 : LpCsa8 : LpCsa1 : LpCsa2 : LpCsa3 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa7 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa8 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa7 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  * 620 * 640 * 660	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa6 : LpCSa7 : LpCSa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  * 620 * 640 * 660	: 12 : - : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa7 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGNGGCGCAAATGA CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa7 : LpCSa7 : LpCSa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGCGCAAATGA CACTGCTCTTTCTGGTGCTGTTTGGAGCTCTATATGGTCCACTGCATGGTGCGCAAATGA CACTGCTCTTTCTGGTGCTGTTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : -
LpCSa5 : LpCSa6 : LpCSa7 : LpCSa1 : LpCSa2 : LpCSa3 : LpCSa4 : LpCSa5 : LpCSa6 : LpCSa6 : LpCSa7 : LpCSa7 : LpCSa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGNGGCGCAAATGA CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : - : -
LpCsa5 : LpCsa6 : LpCsa7 : LpCsa1 : LpCsa2 : LpCsa3 : LpCsa4 : LpCsa5 : LpCsa6 : LpCsa6 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : - : -
LpCsa5 : LpCsa6 : LpCsa7 : LpCsa1 : LpCsa2 : LpCsa3 : LpCsa4 : LpCsa5 : LpCsa6 : LpCsa6 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : - : -
LpCsa5 : LpCsa6 : LpCsa7 : LpCsa1 : LpCsa2 : LpCsa3 : LpCsa4 : LpCsa5 : LpCsa6 : LpCsa6 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa7 : LpCsa8 :	* 560 * 580 * 600  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT  CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT   * 620 * 640 * 660  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA  CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA	: 12 : - : - : - : - : - : 466 : 72 : - : - : - : -

	* 680 * 700 * 720	
Z == 00 = 1	NGCGGTACTT-AAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA	: 719
LpCSa1 : LpCSa2 :	GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA	: 586
LpCSa2 :	GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA	: 192
	GGCGGTACTTAAATGTTAAATGACATTCACACTCACCACTCACCACTCACCACTCACCACTCACCAC	: -
LpCSa4 :		: -
LpCSa5 :		· • -
LpCSa6 : LpCSa7 :	,	: -
LpCSa7 :		: -
прсвае :		
	* 740 * 760 * 780	
LpCSal :	GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGNTTTGGGCACN	: 763
LpCSa2 :	GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA	: 646
LpCSa2 :		: 252
LpCSa4	GGCAGIOAAGARICAGGAIAGAGGAIATTTTTTTTTTTTTTTTTTTTTTTTT	: 2
LpCSa5		: -
LpCSa6		: -
LpCSa7		: -
LpCSa8	***************************************	: -
	* 800 * 820 * 840	
LpCSa1	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	: -
LpCSa2	TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGN	: 682
LpCSa3	TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG	: 312
LpCSa4	TTATCCTCGCGCTAAAGTCAT-CCGCAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG	: 61
LpCSa5	GGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG	: 37
LpCSa6		: -
LpCSa7		· -
LpCSa8	~	: -
	* 860 * 880 * 900	
7 - 60 - 1	* 860 * 880 * 900	
LpCSal		•
LpCSa2		: -
LpCSa3	CCA $TCCTCTCA$ $TCCA$ $CCTA$ $CCTCTTCCCTTTCCA$ $CA$ $A$ $CCTA$ $CCA$ $CTCTCA$ $CA$ $CCA$ $CTA$ $TTT$	: - : 372
T-5-C-C-1	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGTAGCACTGTCAGACGAGTATTT	: - : 372 : 121
LpCSa4	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT	
LpCSa5	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAGGCAGCACTGTCAGACGAGTATTT GGMTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT	: 121
LpCSa5 LpCSa6	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT TNNCAGACGAGTATTT	: 121 : 97
LpCSa5 LpCSa6 LpCSa7	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAGGCAGCACTGTCAGACGAGTATTT GGMTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT	: 121 : 97 : 16
LpCSa5 LpCSa6	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT TNNCAGACGAGTATTT	: 121 : 97 : 16
LpCSa5 LpCSa6 LpCSa7	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT	: 121 : 97 : 16
LpCSa5 LpCSa6 LpCSa7	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT TNNCAGACGAGTATTT	: 121 : 97 : 16
LpCSa5 LpCSa6 LpCSa7 LpCSa8	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT	: 121 : 97 : 16
LpCSa5 LpCSa6 LpCSa7 LpCSa8 LpCSa1 LpCSa2	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT TNNCAGACGAGTATTT GTCAGACGAGTATTT  * 920 * 940 * 960	: 121 : 97 : 16 : 15 : -
LpCSa5 LpCSa7 LpCSa8 LpCSa8 LpCSa1 LpCSa2 LpCSa3	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT TNNCAGACGAGTATTT GTCAGACGAGTATTT  * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT	: 121 : 97 : 16 : 15 : -
LpCSa5 LpCSa6 LpCSa7 LpCSa8 LpCSa1 LpCSa2 LpCSa3 LpCSa4	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : -
LpCSa5 LpCSa8 LpCSa8 LpCSa1 LpCSa2 LpCSa3 LpCSa4 LpCSa5	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : - : 432 : 181 : 157
LpCSa5 LpCSa8 LpCSa8 LpCSa1 LpCSa2 LpCSa3 LpCSa4 LpCSa5 LpCSa5	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa8 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : - : 432 : 181 : 157
LpCSa5 LpCSa8 LpCSa8 LpCSa1 LpCSa2 LpCSa3 LpCSa4 LpCSa5 LpCSa5	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa8 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa8 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6 LpCsa7	# 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTTTTTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6 LpCsa7	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa7 LpCsa1 LpCsa2 LpCsa3 LpCsa4 LpCsa5 LpCsa6 LpCsa6 LpCsa7 LpCsa8	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  - TNNCAGACGAGTATTT GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCCTAATATATAGGGCAAT TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT TATCGAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  * 980 * 1000 * 1020	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa8	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCCTAATATATAT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76 : 75 : -
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa6 LpCsa6 LpCsa7 LpCsa8 LpCsa8 LpCsa1 LpCsa2 LpCsa1 LpCsa2 LpCsa3 LpCsa3 LpCsa3	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76 : 75 : - : -
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa6 LpCsa6 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa2 LpCsa3 LpCsa4 LpCsa3	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGMTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76 : 75 : - : 492 : 492 : 241
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa6 LpCsa6 LpCsa6 LpCsa8 LpCsa1 LpCsa2 LpCsa1 LpCsa2 LpCsa3 LpCsa3 LpCsa3 LpCsa5 LpCsa5	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGMTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT  * 980 * 1000 * 1020  GGGATTCCCTACAGAGTTTTTCCCTGTTTTGCAGTTCCTCGCATGGCTGGTTGGT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76 : 75 : - : 492 : 241 : 217
LpCsa5 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa3 LpCsa6 LpCsa6 LpCsa6 LpCsa7 LpCsa8 LpCsa1 LpCsa2 LpCsa2 LpCsa3 LpCsa4 LpCsa3	GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  GGMTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT  TNNCAGACGAGTATTT  GTCAGACGAGTATTT   * 920 * 940 * 960  TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAT	: 121 : 97 : 16 : 15 : - : 432 : 181 : 157 : 76 : 75 : - : 492 : 241 : 217 : 136

LpCSa1								
LpCSa1				•				•
DPCSA1		*	1040	* .	1060	*	1080	
LpCSa2	ImCSa1 :						:	-
LpCSa3 :         InCCACATTGGAAGGAGTCACTTGATGACCCCGACATMANATTATGAGGCCCCAACAGGT           LpCSa4 :         AGCACATTGGAAGGAGTCACTTGATGACCCCGACATMANATTATGAGGCCCCAACAGGT           LpCSa5 :         AGCACATTGGAAGGAGTCACTTGATGACCCCGACATMANATTATGAGGCCCCAACAGGT           LpCSa7 :         AGCACATTGGAAGGAGTCACTTGATGACCCCGACATMANATTATGAGGCCCCAACAGGT           LpCSa8 :         **** 1100 *** 1120 *** 1140 ***           LpCSa8 :         **** 1100 *** 1120 ***           LpCSa2 :         **** 1100 *** 1120 ***           LpCSa2 :         **** 1100 **** 1120 ***           LpCSa2 :         **** 1100 **** 1120 ***           LpCSa2 :         **** 1100 **** 1120 ***           LpCSa2 :         **** 1700 **** 1120 ****           LpCSa3 :         **** 1700 **** 1120 ****           LpCSa4 :         **** 1700 **** 1120 ****           LpCSa5 :         **** 1700 **** 1120 ****           LpCSa6 :         **** 1700 **** 1120 ****           LpCSa7 :         **** 1700 **** 1120 ****           LpCSa8 :         **** 1160 **** 1180 ****           LpCSa7 :         **** 1160 **** 1180 ****           LpCSa8 :         **** 1160 ***** <td></td> <td></td> <td></td> <td><b>-</b></td> <td></td> <td></td> <td>:</td> <td></td>				<b>-</b>			:	
LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGACATAAAATTATAGAGGCCCAAAGGT   277     LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGACATAAAATTATGAGGCCCCAAAGGT   195     LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGACATAAAATTATGAGGCCCCAAAGGT   195     LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGACATAAAATTATGAGGCCCCAAAGGT   195     LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGACATAAAATTATGAGGCCCCAAAGGT   195     LpCsaf   AGCACATTGGAAGGAGTCACTTGATGACCCCGCCACATAAAATTATGAGGCCCAAAGGT   195     LpCsaf   ATACACCGGTACTTGGTAAAGGCATTACACCCCAGTGAAGAAACGGTGCATCAAGCG   6612     LpCsaf   ATACACCGGTACTTGGTAAAGGCATTACACCCCAGTGAAGAAACGGTGCATCAAGCG   361     LpCsaf   ATACACCGGTACTTGGCTAAAGGCATTACACCCCAGTGAAGAACCGGTGCATCAAGCG   225     LpCsaf   ATACACCGGTACTTGGCTAAAGGCATTACACCCCAGTGAAGAACCGGTGCATCAACCG   225     LpCsaf   ATACACCGGTACTTGGCTAAAGGCATTCAAACCGAGAGAACCGGTGCGATCACTCAACCGA   225     LpCsaf   ATACACCGGTACTTGGCAGATCGCTCACACCAAAACCGAAGAACCGAGCGTCGGCATCAACCGA   225     LpCsaf   ATACACCGGTACTGCAGATCGCTCACACCAAAACCGAAGAACCGAGGCGTCGGCGTGCATCAACCGA   225     LpCsaf   ATACACCGGTACGCTCGACTCAAAACCGAAACCGAAACCGAACCGAGCGTCGGCGTGCATCAACCGAACCAAAACCAAAACCGAACGAGACCGTCGAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA		AGCACATTGGAAGC	SAGTCACTTGATO	SACCCCGAC	AATAAAATTA	TGAGGCCCCA	ACAGGT :	
LpCSa5   AGCACATTGGAAGGAGTCACTTGATGACCCCACCATATATAT		ACCACATTCCAAGO	PACTCACTTGATO	FACCCCGAC	AATAAAATTA	TGAGGCCCCA	ACAGGI :	
LpCSa1		ACCACATTCGAAGO	AGTCACTTGAT	SACCCCGAC	ATTAAAATTA	TGAGGCCCCA	VA(CA(GGT :	
LpCSa1		ACCACATTGGAAG	PAGTCACTTGATO	SACCCCGAC	ATTAAAATTA	TGAGGCCCCA	AACAGGT :	
LpCSa1		AGCACATTGGAAG	GAGTCACTTGAT	GACCCCGAC	AATAAAATTA	TGAGGCCCCA	ACAGGT :	195
Table							:	-
LpCSa1 :								
LpCSa1 :						_	3340	
LpCSa3 : ATACACCGGTACTTGGCTAAGGCATTACACCCCASTGAGAGAACGGGTGCCATCAAGCGA : 612 LpCSa4 : ATACACCGGTACTTGGCTAAGGCATTACACCCCASTGAGAGAACGGGTGCCATCAAGCGA : 361 LpCSa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCASTGAGAGAACGGGTGCCATCAAGCGA : 337 LpCSa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCASTGAGAGAACGGGTGCCATCAAGCGA : 255 LpCSa7 : ATACACCGGTACTTGGCTAAGGCATTACACCCCASTGAGAGAACGGGTGCCATCAAGCGA : 255 LpCSa8 :		*	1100	*	1120	*	1140	-
LpCsa3 : ATACACCGTACTTGGCTAAGGCATTACACCCCAGTAGAGAAGGGGTGCCATCAAGCGA : 361 LpCsa5 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAAGGGGTGCCATCAAGCGA : 337 LpCsa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAAGGGTGCCATCAAGCGA : 255 LpCsa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 255 LpCsa7 : ATACACCGGTACTTGGCTAAGGCATACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 255 LpCsa8 :  * 1160 * 1180 * 1200  LpCsa1 :							:	-
LpCSa3 : ATACACCGGTACTTGCTAAGGCATTACACCCAGTGAGAAACGGGTGCCATCAAGCGA : 361 LpCSa5 : ATACACCGGTACTTGCTAAGGCATTACACCCCAGTGAGAAACGGGTGCCATCAAGCGA : 256 LpCSa6 : ATACACCGGTACTTGGTAAGGCATTACACCCCAGTGAGAACGGGTGCCATCAAGCGA : 256 LpCSa7 : ATACACCGGTACTTGGTAAGGCATTACACCCCAGTGAGAAACGGGTGCCATCAAGCGA : 256 LpCSa8 :					CTCACACAA	CCCTCCCATC	CAAGCGA	612
LpCSa5		ATACACCGGTACT	TGGCTAAGGCA'I"	TACACCCCF	CTCACACAAAC	CCCTCCCAT(	CAAGCGA:	-
LpCSa5 : ATACACCGTACTTGCTAAGGCATTACACCCCACTGAGAGAACGGGTGCCATCAAGCGA : 256 LpCSa7 : ATACACCGTACTTGCCTAAGGCATTACACCCCACTGAGAGAACGGGTGCCATCAAGCGA : 255 LpCSa8 :  * 1160 * 1180 * 1200  LpCSa1 :		ATACACCGGTACT	TGGCTAAGGCAT	TACACCCCA	CTCACACAAC	CCCTCCCAT	CAAGCGA	
LpCsa6		ATTACACCGGTACT	TGGCTAAGGCAT	TACACCCCA	GTGAGAGAAC	CGGTGCCAT	CAAGCGA	_
LpCsa1		ATTACACCGGTACT	TGGCTAAGGCAT	TACACCCCA	CTGAGAGAAC	CGGTGCCAT	CAAGCGA :	
# 1160 * 1180 * 1200  LpCSa1 :		AVVACACCGG IVACT	IGGCIAAGGCAT	LACACCCC				-
LpCSa1 :	rbcsa8 :							
LpCSa1 :								
LpCSa3 : CAGTGAGCAGCTTGGGCAGATCACTCATCAAACGCGACGAGGCGTCGGCTGCTGCTC : 672 LpCSa4 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGGCTCGGCTGGCT		*	1160	*	1180	*	1200	
LpCSa3 : CAGTGAGCAGCTTGGGCAGATCACTCATCAAACGCGACGAGGCGTCGGCTGCTGCTC : 672 LpCSa4 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGGCTCGGCTGGCT	LpCSa1 :						;	-
LpCsa3 : CAGTGAGCAGCTTGGGCAGATCGCTTACATCAAACGCGACGAGGGCTTCGGCTGGTTGTTC : 421 LpCsa5 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGGCTTCGGCTGGCT								
LpCSa4 : cAGTGAGCAGCTTGGGCAGATCCCTACATCAAACGCGACGAGCGTCGGGTGTGGGTGTGGTGTC : 3297 LpCSa5 : CAGTGAGCAGCTTGGGCAGATCCCTACATCAAACGCGACGAGGGGTGGGGTGTGGGTC : 316 LpCSa7 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTTCGGCTTCGTCTC : 315 LpCSa8 :		CAGTGAGCAGCTI	GGGCAGATC <mark>A</mark> CT	ACATCAAA	CGCGACGAGG	CGTCGGCGTG	CTGGITC :	
LpCsa6		CACTGAGCAGCTT	GGGCAGATCGCT	'ACATCAAA	CGCGACGAGG	CGTCGGCGTG	CIGGCIC	
LpCSa6 : AGTGAGCAGCTTGGGCAGATCGCTACATCAAACCGGACGAGGGCTCGCGTCTGGCTC : 315 LpCSa7 : CAGTGAGCAGCTTGGGCAGATCGCTTCATACACCGGACGAGGGGTCGGCTGGCT		CAGTGAGCAGCTT	GGGCAGATCGCT	'ACATCAAA	CGCGACGAGG	CGTCGGCGTG	CIGGCIC	
LpCSa1: CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACCGCAGCGAGGCGTCGGCTGCTGCTC : 45  LpCSa8:		CAGTGAGCAGCTT	GGGCAGATCGCT	'ACATCAAA	CGCGACGAGG	CGTCGGCGTG	CIGGCIC	
* 1220 * 1240 * 1260  LpCSa1 :		CAGTGAGCAGCTT	CCCCAGATCGCT	ACATCAAA	CGCGACGAGG	CGTCGGCGTG	GIGGGIG	
LpCSa1: LpCSa2: LpCSa3: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA			-GGCAGATCGCT	-CATCAAA	CGCGTCGAGG	CGTCGGCGTG	CTGGCTC	: 45
LpCSa1: LpCSa2: LpCSa3: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA	-							
LpCSa1: LpCSa2: LpCSa3: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA							1260	
LpCsa2 : LpCsa3 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCACAATAAACCAAGCTGCCA : 732 LpCsa4 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCACAATAAACCAAGCTGCCA : 481 LpCsa5 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCAATAAACCAAGCTGCCA : 487 LpCsa6 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCAATAAACCAAGCTGCCA : 376 LpCsa7 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCAATAAACCAAGCTGCCA : 375 LpCsa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCAATAAACCAAGCTGCCA : 375 LpCsa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACCAATAAACCAAGCTGCCA : 375 LpCsa1 : LpCsa2 : LpCsa3 : AGGGCCACGGCTGCTTAAATCTGGAACTACAGTCCACCAATAAACCAAGCTGCCA : 105  LpCsa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA		*	1220	*	1240			
LpCsa4: TGCCCTGTAGAACAGTCTGCATGATACAGCATTACAGTCCACACAATAAACCAAGCTGCCA: 481 LpCsa5: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 487 LpCsa6: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 457 LpCsa6: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 376 LpCsa7: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 375 LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 375 LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA: 105  LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGCTCACACAATAAACCAAGCTGCCA: 105  LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGGCTACACAATAAACCAAGCTGCCA: 105  LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGGCTACACACAATAAACCAAGCTGCCA: 105  LpCsa1: LpCsa2:								: -
LpCsa4 : TGCCCTGTAGAACAGTCTGCATGATACAGCATCACACACA		та са стата съ	A CTCTCCATCAT	гасассата	CAGTCCACAC	AATAAACCAA	GCTGCCA	: 732
LpCsa5 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 457 LpCsa6 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 376 LpCsa7 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 375 LpCsa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 105  * 1280 * 1300 * 1320  LpCsa1 :	_	TGCCCTGTAGAAC	AGICIGCAIGAI	CACAGCATA	CAGTCCACAC	AATAAACCAA	GCTGCCA	: 481
LpCsa6: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACAATAAACCAAGCTGCCA : 375 LpCsa7: TGCCCTGTAGAACAGTCTGCATGATACAGCATCCACCAATAAACCAAGCTGCCA : 375 LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGCATCCACCAATAAACCAAGCTGCCA : 105  * 1280 * 1300 * 1320  LpCsa1:	_	TGCCCTGTAGAA	AGICIGCAICA:	PACAGCATA	CAGTCCACAC	AATAAACCAA	GCTGCCA	: 457
LpCsa7 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGGTGCCA : 375 LpCsa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 105  * 1280 * 1300 * 1320  LpCsa1 :	-	TCCCCTCTAGAA	CACTCTGCATGAT	CACAGCATA	CAGTCCACAC	AATAAACCAA	GCTGCCA	
LpCsa8: TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACAATAAACCAAGCTGCCA : 105  * 1280 * 1300 * 1320  LpCsa1:		TCCCCTCTAGAA	PAGTCTGCATGAT	PACAGCATA	CAGTCCACAC	AATAAACCA#	AGCTGCCA	
LpCSa1: LpCSa2: LpCSa3: AGGGCACGGCTGCTTAAATN—		TGCCCTGTAGAA	AGTCTGCATGA	TACAGCATA	CAGTCCACAC	AATAAACCAA	GCTGCCA	: 105
LpCsa2: LpCsa3: AGGGCCACGGCTGCTTAAATN	חהרפמס	. IOCCCIOINOM						
LpCsa2: LpCsa3: AGGGCCACGGCTGCTTAAATN								
LpCsa2 : LpCsa3 : AGGGCCACGGCTGCTTAAATN  LpCsa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATAT LpCsa5 : AGGGCCACACGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA		. *	1280	*	1300	*	1320	
LpCsa3 : AGGGCCACGGCTGCTTAAATN : 753  LpCsa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATGTAGGC : 541  LpCsa5 : AGGGCCACACGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA		:						
LpCsa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATCTAGGC LpCsa5 : AGGGCCACACGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA	LpCSa2	:						. 753
LpCsa5 : AGGGCCACAGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA	LpCSa3	: AGGGCCACGGCT	GCTTAAATN		ma ormanare	ATCACCTATI	ATCTACCC	
LpCsa5 : AGGCCACAGCIGCITAAATCIGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC LpCsa6 : AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA		: AGGGCCACGGCT	GCTTAAATCTGG(	GAGCTGCTA	TACTIGIGIL	AICACGIAIA ATCACCTATA	TATAGGC	: 517
LpCsa6 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATA		: AGGGCCACAGCT	GCTTAAATCTGG	CAGCIGCIA	TACIIGIGII	ATCACGTATA ATCACGTATA	TATAGGC	
* 1340 * 1360 * 1380  LpCsa1: LpCsa2: LpCsa3: LpCsa3: LpCsa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa7: AATAAACTAATAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSa7: AATAAACTAATAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSA7: AATAAACTAATAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSA7: AATAAACTAATAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSA7: AATAAACTAATAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSA7: AATAAACTAATAATAATGCCGCCAAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LPCSA7: AATAAACTAATAATGCTGTGAAGTTGGTAGTAGTAGAAGTTGGTAGTAGAAGTTGGTAGTA		: AGGGGGACGGCII	GCTTAAATCTGG	SAGCIGCIA	TACTIGIGIT	PATCACGTATA	ATATAGGC	
* 1340 * 1360 * 1380  LpCsa1: LpCsa2: LpCsa2: LpCsa3: LpCsa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCsa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 496		: AGGGGCACGGCII	GCTTAAATCTGG	CAGCIGCIA	TAC1 1G1G11	PATCACGTAT	ATATAGGC	
LpCSa1: LpCSa2: LpCSa3: LpCSa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 496 LpCSa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 497	LpCSa8	: AGGGCCACGGCT	GCTTAAATCIGG	CAGCIGCIA	71WC11G1G11	cc		
LpCSa1: LpCSa2: LpCSa3: LpCSa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 496 LpCSa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 497								
LpCSa2: LpCSa3: LpCSa3: LpCSa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA LpCSa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA 496		*	1340	*	1360	*	1380	
LpCsa2:  LpCsa3:  LpCsa4: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA  LpCsa5: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA  LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA  LpCsa6: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA  LpCsa7: AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA  496	LpCSal	:						: -
LpCsa3 :								: -
LpCsa4 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 601 LpCsa5 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 577 LpCsa6 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496 LpCsa7 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496	T DOCA 2							: -
LpCsa5 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 377  LpCsa6 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496  LDCsa7 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 495	LpCSa4	ΑΤΑΑΤΌΑΑΤΟΑΑΤΑ	ATGCCGCCAGGA	CACTTCAC	rggtggtcat(	ETGAAGTTGG'	TAGTAGAA	
LPCSa6 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496		AATAAACTAATA	ATGCCGCCAGGA	CACTTCAC	rggtggtcatc	STGAAGTTGG	TAGLAGAA	
INCORP. AND AN CITA THE ATTECCECCAGGACACTICACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 495		AATAAACTAATA	ATGCCGCCAGGA	CACTTCAC'	rggtggtcat(	gtgaagttgg'	TAGTAGAA	
Lpcsa8 : Aataaactaataatgccgccaggacacttcactggtggtcatgtgaagttggtagtagaa : 225		AATAAACTAATA	ATGCCGCCAGGA	CACTTCAC'	rggtggtcat(	STGAAGTTGG'	TAGTAGAA	
		: AATAAACTAATA	ATGCCGCCAGGA	CACTTCAC	TGGTGGTCAT	STGAAGTTGG	IVAG IVAGAVA	: 225

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			*	1400	*	1420	*	1440	
LpCSa1	:							:	_
LpCSa2	:							:	-
LpCSa3	:							:	-
LpCSa4	:			TTGTTAATTTGTT?					661
LpCSa5	:	TGCACTTG	TAACGTG'	TTGTTAATTTGTT?	ATCCTGC?	AATGTACGCTCTA	TAAACTG:	FTCAG:	637
LpCSa6	:			ITGTTAATTTGTT <i>I</i>					556
LpCSa7	:	TGCACTTG	TAACGTG'	TTGTTAATTTGTT	ATCCTGC	AATGTACGCTCTA	TAAACTG'	TTCAG :	555
LpCSa8	:	TGCACTTG	TAACGTG'	TTGTTAATTTGTT	ATCCTGC	AATGTACGCTCTA	TAAACTG	TTCAG:	285
			*	1460	*	1480	*	1500	
LpCSa1	:							:	-
LpCSa2	:							:	-
LpCSa3	:							:	
LpCSa4	:	TETCTTGA	AAGTCTT	AATCATGTGGACC	AA-GAAGA	ACATAGATCAAGT	TCTTTGC	ATGGG :	720
LpCSa5	:			ANTIC CNNNNA AAA				:	666
LpCSa6	:	TATCTTGA	AAGTCTT	AATCATGTGGACC?	AA-GAAGA	ACATAGATCAAGT	TCTTTGC	Andee :	615
LpCSa7	:			AATCATGTGGACC?	AATICAAA	AAAAAA		:	597
LpCSa8	:	TATCTTGA	AAGTCTT	AAAAAAA				:	310
			*	1520	*	1540	*		
LpCSal	:						: .	-	
LpCSa2	:						:	-	
LpCSa3	:						:	-	
LpCSa4	:	CGGCGGCT	GTTTCTT	rgg <mark>n</mark> aaaaaa			: 749	5	
LpCSa5	:						:	-	
LpCSa6	:	CGGCGGCT	GTTTCTT	igtettettet	TTATGG	SAGTCTTTTTTA	CC : 665	5	
LpCSa7	:						: .	-	
LpCSa8	:							_	

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LpCSb	:	* 20 * 40 * 60 CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG	:	60
LpCSb	:	* 80 * 100 * 120 TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC	:	120
LpCSb	:	* 140 * 160 * 180 CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT	:	180
LpCSb	:	* 200 * 220 * 240 ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG	:	240
LpCSb	:	* 260 * 280 * 300 CTAATTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT .	:	300
LpCSb	:	* 320 * 340 * 360 ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG	:	360
LpCSb	:	* 380 * 400 * 420 TTGGAAGTGCTCTGTCAGATCCTTATCTTTTTTTTTTTT	:	420
LpCSb	:	* 440 * 460 * 480 GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTNATGGATCAAATCTGTGATGGAAG	:	480
LpCSb	:	* 500 * 520 * 540 AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA	:	540
LpCSb	:	* 560 * 580 * 600 GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT	:	600
LpCSb	:	* 620 * 640 * 660 CGTGCCAAAGGAGTTTGCACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT	:	660
LpCSb	:	* 680 * 700 * 720 CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT	:	720
LpCSb	:	* 740 * 760 * 780  GGCCTAATGTTGATGCTCACCAGTGGAGTTTGCTCAACCACTTCGGATTAGTTGAAGCAC	:	780
LpCSb	:	* 800 * 820 * 840 GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT	:	840
LpCSb	:	* 860 * 880 * 900  GGGACCGTGCCCTCGGCCTGCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG	:	900
LpCSb	:	* 920 * 940 * 960 AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG	:	960

980 \* 1000

LPCSb : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 1020

1060 1040

LpCsb : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 1080

1120 1100

LpCsb : CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 1140

1160

LpCSb : GACACATAAGTTTTATGTGTCGCTCGG : 1167

			*	20	*	40	*	60		
LpCSb	:	SPCXCSPMT	QFTTGVMA	LQVESEFAKAYE	KGIHKSKF	WEPTYEDSLNL	IARLPQVAS	YVY	:	60
			*	80	*	100	* ~~\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	120		120
LpCSb	:	RRIFKDGKT	TAADNTLD	YAANFSHMLGFD	DEKMTEPA	KUIIIIINNE	GGNVSANAC	MIN	•	120
				140	* .	160	*	180		
LpCSb	:	GSALSDPYL	SFAAALNG	LAGPLHGLANQE	VLXWIKSV	MEETGSNITTD	<b>OLKEYVWKI</b>	rlks	:	180
			*	200	*	220	*	240		
LpCSb	:	GKVVPGYGH		RYSCOREFALKY	LPEDPLFO	)LVSKLYEVVPP	ILTELGKVF	MPW	:	240
				260	*	280	*	300		
LpCSb	:	PNVDAHSGV		earyytvlfgvs	RSMGIGS		ERPKSVTME	-	:	300

Lpcsb : NHCKKAAA : 308

ure 6 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSb

		* 20 * 40 * 60	
LpCSb1	:	CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG	: 60
LpCSb2	:		: -
LpCSb3	:		: -
LpCSb4	:		: -
TP COD 1	•		
		± 80 .* 100 * 120	
Lacchi	:		: 120
LpCSb1	•	ITGAGAGTGAATTTGCAAAGGCTTATGAGAAAGGGAATTG	
LpCSb2	:		
LpCSb3	:		-
LpCSb4	:		•
		* 140 * 160 * 180	
		* 140 * 160 * 180 CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT	: 180
LpCSb1	:	CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT	. 100
LpCSb2	:		
LpCSb3	:		-
LpCSb4	:		• -
		· * 200 * 220 * 240	
		ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG	: 240
LpCSb1	:		
LpCSb2	:		
LpCSb3	:		
LpCSb4	:		: -
		* 260 * 280 * 300	
		* 260 * 280 * 300 CTAATTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT	: 300
LpCSb1			. 505
LpCSb2	:		: -
LpCSb3	:		
LpCSb4	:		• -
		* 320 * 340 * <u>360</u>	
T OCh 7			: 360
LpCSb1			
LpCSb2			-
LpCSb3			
LpCSb4	:		•
		* 380 * 400 * 420	
LpCSb1		TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG	: 420
LpCSb2			: -
LpCSb3			: -
LpCSb4			: -
TPC004	•		
		* 440 * 460 * 480	
LpCSb1		GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTTATGGATCAAATCTGTGATGGAAG	: 480
LpCSb2		TNATGGAT - NATCTGTGATGGAAG	: 24
LpCSb3			: -
LpCSb3			: -
Theona	•		
		* 500 * 520 * 540	
LpCSb1	. :	AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA	: 540
LpCSb2		<ul> <li>AACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA</li> </ul>	: 83
LpCSb3		CTGAAGA	: 7
LpCSb4			: -
	-		

					500	•	600	
		*	560		580			600
LpCSb1:	GTGGAAAG	STTGTTCCT	GGCTATGGTCA	TGGAGTTC	TACGTAATACAC	TATCCACGAT	ACT :	143
LpCSb2:	GTGGAAAG	GTTGTTCCT	GGCTATGGTCA	TGGAGTIC	TACGTAATACAC	PATCCACGAT	ACT	67
LpCSb3:	GTGGAAAG	GTTGTTCCT	GGCTATGGTCA	TGGAGT I.C	TACGTAATACAC	BAICCACGAI	ACT .	-
LpCSb4 :							• •	-
						•		
			620		640	*	660	
z gg\-a	GCTGGGA A	A CCC A CTTTT		TTTACCIG	AAGACCCACTT	TTCCAACTGG		660
LpCSb1:	CGTGCCAA	AGGGAGIII ACCCACTTT	CCACTGAAGTA	TTTACCEG.	AAGACCCACTT	TTCCAACTGG	TCT :	203
LpCSb2 :	CGTGCCAA	AGGGAGIII	CNIACTER ACTA	0000011	AAGACCCACTT	TCCAACTGG	тст :	127
LpCSb3 : LpCSb4 :	CGIGCCAA	AGGGAGI	CWACTCALCIA				:	-
npcsp4:								
						•		
		*	680	*	700	*	720	
LpCSb1 :	CCAAGTTG	TATGAAGTT	GTGCCTCCTAT	CCTCACTG	AGTTAGGCAAG	STAAAAAACC	CAT :	720
LpCSb2 :	CCAAGTTG	TACGAAGTT	TGTGCCTCCTAT	CCTCACCG	AGTTAGGCAAG	GTAAAAAACC	CAT:	263
LpCSb3 :	CCAAGTTG	TACGAAGTI	GTGCCTCCTAT	CCTCACCG	AGTTAGGCAAG	GTAAAAAACC	CAT:	187
LpCSb4 :							:	_
		* .	740	*	760	*	780	
LpCSb1 :	GGCCTAAT	GTTGATGCT	CACAGNIGGAGT	TTTGCTCA	ACCACTTCGGA'	TTAGTTGAA-	CAC :	779
LpCSb2	GCCTAAT	GTTGATGCT	CACAGTGGAGT	TTTGCTCA	ACCACTTCGGA	TTAGTTGAAG	CAC:	323
LpCSb3	GGCCTAAT	GTTGATGCT	CACAGTGGAGT	TTTGCTCA	ACCACTTCGGA	TTAGTTGAAC	CAC:	247
LpCSb4							:	-
			000		820	•	840	
I mochi	CCMACTAC	ACTGNCTTC	800	. <b></b> .			:	802
LpCSb1 LpCSb2	GGNACIAC	ACIGNCIIC ACTGTCTT	TTTCGCCGTCTC	CAAGGAGCA	TGGGAATTGGA	TCTCAGCCC	ATTT	383
LpCSb2	GGTACTAC	'ACTOTOTO	TTCGGCGTCTC	CAAGGAGCA	TGGGAATTGGA	TCTCAGCTCA	TTT:	307
LpCSb4	Germen				GTTTTTGGA	TCCCAGCTC	ATTT :	22
Dp CCD 1								
		*	860	*	880	*	900	_
LpCSb1				7707007	AGAGTGTCACC	ATCCACTCC	TOCC .	443
LpCSb2	GGGAGGG	GCCCTCGG	CCTGCCACTTGA	AAAGACCGA	AGAGTGTCACC AGAGTGTCACC	ATGGAGTGG ATGGAGTGG	TEG:	367
LpCSb3	eee Acces	GCCCTCGG	CCTGCCACTTGA	AAAGACCGA	AGAGTGTCACC	ATGGAGTGG	TGG:	82
LpCSb4	GGGTCCG.	GCCCTCGG	CCIGCCACIIGA	Minoriccor	THOMOTOT CITED			
		*	920	*	940	*	960	
LpCSb1	:							- 503
LpCSb2	: AAAACCAC	CTGCAAGAA	GGCTGCGGCCT	BAAGCTACA	ACCAATGCTTCG	TTTTACAAA.	TCAG:	427
LpCSb3	: AAAACCAC	CTGCAAGAA	GGCTGCGGCCTC	SAAGCTACA	ACCAATGCTT <mark>N</mark> G ACCAATGCTTCG	TTTTACAAA.	CAG:	
LpCSb4	: AAAACCAC	TGCAAGAA	GGCTGCGGCCTC	SAAGCIACA	ACCAMIGCTICG	IIIIACAAA	. c.r.c	
		*	980	*	1000	*	1020	
LpCSb1	:						;	
LpCSb2	: GCCGTCT	TGATGTTA	ATAATGACTGAG	GCATAAGT:	PAGGCATGGTTA	GCCTTGTTT	PACC:	563
LpCSb3	: GCCGTCT	TGATGTTA	ATAATGACTGA	GCATAAGT'	raggcatgg <mark>g</mark> ta	GCCTTGTTT	PACC:	487 202
LpCSb4	: GCCGTCT	TGATGTTA	ATAATGACTGA	5CATAAGT	raggcatggTTA	GCCTTGTTT	-ACC	202
		*	1040	*	1060	*	1080	
LpCSb1	:						:	-
LpCSb2	: ATCTTCG	TTTTCCTGG	CCAATAACTGG	AGCAAGAG	GCT <mark>T</mark> ACAGACGC	TAGAATTTT	GTAA :	623
LpCSb3	: ATNITTCG	TTTTCCTGG	CCAATAACTGG.	AGCAAGAG	GCTCACAGACGO	TAGAATTTT	GTAA :	547
LpCSb4	: ATCTTCG	TTTTCCTGG	CCAATAACTGG	AGCAAGAG	GCTCACAGACGG	TAGAATTTTT	GIVAVA :	262

.

\* 1100 \* 1120 \* 1140

LpCsb1:

LpCsb2: CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 683

LpCsb3: CCACCGCTACTTG\_ACACCGAATNANNTAAATGCNATTTGGCATAAAGAGATTAGGACAT : 606

LpCsb4: CCACCGTTACTTGAACACCGAATCAGTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 322

1160

7-00-		* TCNCCGTGGCCANAATN	20 100000000000000000000000000000000000	* አልተልሮርር(	40 CCGTCAGCCAC	* CAATCCTC	60 CTAC		60
ppcse	:	TCNCCGTGGCCANAATA	·	-MATING CO.				•	
	•	*	80	*	100	*	120		120
LpCSc	:	CTTCTTATTTCCACCCC	CAACCGCCCAAC	ATGTGTCC	ICCCACCGAANA	MACACCIG	CIAC	•	120
		*	140	*	160	* .	180		
LpCSc	:	CAACGGCCATAGCAACG	GCACCAACGGC	GCCAATGG(	CTCCAAGGAAGG	CTTCACAG	GCGT	:	180
		*	200 .	*	220	*	240		
LpCSc	:	CACGACCAGACAGAACO	CCTCACCCTACA	CACAAGAG	CCCATATGCACO	CTGTTGGCG.	ACTT	:	240
		*	260	*	280	*	300		
LpCSc	:	TTTGTCAAATGTCGGC	CGCTTCAAGATT	ATCGAGAG	CACATTAAGAGI	AGGGCGAGC.	AATT	:	300
		*	320	*	340	*	360		
LpCSc	:	CGCCAACGCCTACTTCC	SACCTTGAGGCT.	AAAATCAA	GATCGCCAGAG	CTCTCGACA	ACTT	:	360
		*	380	*	400	*	420		
LpCSc	:	TGGTGTTGACTACATTC	GAAGTTACCAGC	CCTGCTGC	CTCTGAGCAGT(	CAAGAAGGG	ACTG	:	420
		*	440	*	460	*	480		
LpCSc	:	CGAAGCCCTCTGCAAG	CTCGGATTGAAA	GCCAAGAT	CCTTACCCACG	racgatgcc	ACAT	:	480
		*	500	*	520	*	540		
LpCSc	:	GGACGATGCCAGAATC	GCTGTCGAGACT	GGTGTTGA	CGGCCTCGATG	<b>rcgtcattg</b>	GAAC	. <b>:</b>	540
		*	560 ·	*	580	*	600		
LpCSc	:	CTCTGCGTACCTCCGC	GAGCACAGCCAT	GGCAAGGA	CATGACATACA'	rcaaaaaca	CAGC	:	600
		. ·	620	*					
LpCSc	:	GCTGGAGGTGATTGAG'	TTTGTCAAGAGC	AAGGGAN	: 635				

\* 20 \* 40 \* 60 LpCsc : XRGXNXPXFKYRPSATNPPTFLFPPQPPNMCPPTEXTPATNGHSNGTNGANGSKEGFTGV : 60

\* 80 \* 100 \* 120

Lpcsc : Ttrqnphpthkspyapvgdflsnvgrfkiiestlregeqfanayfdleakikiaraldnf : 120

\* 140 \* 160 \* 180

Lpcsc : GVDYIEVTSPAASEQSRRDCEALCKLGLKAKILTHVRCHMDDARIAVETGVDGLDVVIGT : 180

\* 200 \*

Lpcsc : Saylrehshgkdmtyikntaleviefvkskg : 211

LpCsd	:	* GTGNTATGGCNCANCCAG	20 * NANTCCTNCGTNC	40 CTGGCTNCCAN	* ANNAGNAANAAGCT.	60 ATCGG		60
		•					•	
LpCsd	:	* CAACGACCTCAGCGATCA	80 * GGCCATCAAGGAC	100 CTACCTGTGGT	* CCACCCTCAAGGCT	120 GGCCA	:	120
		* 1.	40 *	160		100		
LpCSd	:	AGTCGTTCCCGGTTACGG			ACCCCGCTACGTC	180 TCCCA	:	180
			00 *	220	*	240		
LpCSd	:	GCGCGAGTTCGCCCAGAA	GCACCTTCCCGAC	'GACCCAATGTI	CAAGCTCGTCAGT	CAGGT	:	240
LpCSd	:	* 20 CTACAAGATCGCCCCTGG	50 * የGጥጥርጥር እርር ር እር	280	* ************************************	300		300
			1011010nc	CACOCCARGAC	CANGANCCCCIAC	CCAM	•	300
LpCsd	:	* 32 CGTCGACGCCCACTCCGG	20 * FGTCCTCCTCCAG	340 TACTACGGCCT	* CACTGAGCAGAAC	360 FACTA	:	360
		* 31	30 *	400	*	420		
LpCSd	:	CACCGTTCTCTTCGGTGTA			CCAGCTTATCATT		:	420
I = CD4		* 44		460	*	480		
upcsa	:	TGCCGTCGGTGCCCCATT	'GAGAGGCCCAAG	TCTTTCAGCAC	TGAGGCTTACGCC	AAGTT	:	480
LpCSd	:	* 50 GGTTGGTGCTAÄGTTGTAA		520 AACGTGCTCTA	.CAGCCAGGAGAATG	540 ETGGA	:	540
						•		
LpCSd	:	* 56 GGAATTTGTTTAACATTCA	-	580 CCTGTGTAGAA	* .TTGCAATGTAAGGA	600 TAGG	:	600

\* 620 \* LpCSd : GAATGGGAGCGTTACGGCGCTACATCACTACATTIN : 636

### gure 10 Deduced amino acid sequence of LpCSd

\* 20 \* 40 \* 60 LpCsd : XYGXXXXPXXWXPXXXXAIGNDLSDQAIKDYLWSTLKAGQVVPGYGHAVLRKTDPRYVSQ : 60

\* 80 \* 100 \* 120

LpCsd : REFAQKHLPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEQNYY : 120

\* 140 \* 160

Lpcsd : TVLFGVSRALGVLPQLIIDRAVGAPIERPKSFSTEAYAKLVGAKL : 165

LpMDHa :	* GGTTGGTTGCTGGT	20 TATCACCATTO	* TGCCCTGTI	40 CTCACAGGCA	* ACTCCTTCGA	60 CTAATGC	:	60
LpMDHa :	* ATTGTCTAGTGAAG	80 SACATCAAGGC	* TCTCACCAA	100 .GAGGACACAG	* GAGGGTGGGA(	120 CAGAAGT	:	120
LpMDHa :	* TGTTGAGGCAAAGG	140 CTGGAAAGGG	* ATCTGCAAC	160 CTTGTCCATG	* GCGTATGCTG(	180 GCGCAGT	:	180
LpMDHa :	* TTTTGGTGATGCAT	200 GCTTGAAGGG	* TCTGAACGG	220 AGTTCCTGAC	* ATTGTTGAAT(	240 ECTCCTA	:	240
LpMDHa :	* CGTGCAATCAACTA	260 TCACAGAACT	* GCCATTCTT	280 TGCCTCCAAG	* GTGAGGCTCGC	300 GGAAGAA	:	300
LpMDHa :	* TGGAGTCGAGGAAG	320 TGCTTGGTTT	* GGGTGAGCT	340 GTCGGCCTTT(	* Gagaaggaagg	360 STTTGGA	:	360
LpMDHa :	* AAGTCTCAAGGGTG	380 AGCTCAAGTC	* TTCAATTGA	400 CAAGGGCATC	* GCGTTCGCCAP	420 ATGCGAG	:	420
LpMDHa :	* TTAATTAATTTTGC	440 AGATTATAGC	* AAACCAGGT(	460 CTAGTTAAGGG	* GTCTGTTTT	480 GACTTT	:	480
LpMDHa :	* TTGTTCAGTGCTTT	500 TTCTGCCCAT(	* Cacgtgggci	520 ATGGAAGATT	* FGAGCTTCACA	540 ATAAAA	: :	540
LpMDHa :	* ATCCGGCGGCGTAA	560 TGCCACAGAA(	* CATTACTTG:	580 FACAAGAGGG#	* AACTAGTTCGT	600 GTCAAG	: (	600
LpMDHa :	* TTTTGAACTGGTAC		* Caattgetg <i>i</i>	640 ATGCACTTTGF	* AGAAAAAAAAA	660 TTGGGG :	: (	660
LpMDHa :	* GTGANTCCATTGGC	680 CTCAAGCCAAA	* \$&&&&&&&	AAA : 696				

# Deduced amino acid sequence of LpMDHa

LpMDHa : VGCWYHHSALFSQATPSTNALSSEDIKALTKRTQEGGTEVVEAKAGKGSATLSMAYAGAV : 60

LpMDHa : FGDACLKGLNGVPDIVECSYVQSTITELPFFASKVRLGKNGVEEVLGLGELSAFEKEGLE : 120

LpMDHa : SLKGELKSSIDKGIAFANAS : 140

gure 13 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHa

		* 20 * 40 * 60		
LpMDHa1	:	GITTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC	:	60
LpMDHa2	:	-GETGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC	:	59
LpMDHa3	:	-GTGGECTGCTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC	:	59
LpMDHa4	:	GGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC	:	56
LpMDHa5	:		:	-
LpMDHa6	:		:	-
LpMDHa7	:		:	-
		* 80 * 100 * 120		
LpMDHa1	:	ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT	:	120
LpMDHa2	:	ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT	:	119
LpMDHa3	:	ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT	:	119
LpMDHa4	:	ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT	:	116
LpMDHa5	:	GAGGGTGGGACAGAAGT	:	17
LpMDHa6	:			_
LpMDHa7	:	***************************************	:	_
-			-	
		* 140 * 160 * 180		
LpMDHa1	:	TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT	:	180
LpMDHa2	:	TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT	:	179
LpMDHa3	:	TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT	:	179
LpMDHa4	:	TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT	:	176
LpMDHa5	:	TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT	•	77
LpMDHa6	:		•	· · <u>·</u>
LpMDHa7	:		÷	_
	•		•	
		* 200 * 220 * 240		
LpMDHa1	:			240
LpMDHa1 LpMDHa2	:	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	:	240 239
LpMDHa2	: :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	:	
LpMDHa2 LpMDHa3	: : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : :	239
LpMDHa2 LpMDHa3 LpMDHa4	: : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5	: : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : :	239 239
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6	: : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260	: : : : : :	239 239 236
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA	: : : : :	239 239 236 137
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7	: : : : : : : : : : : : : : : : : : : :	TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300 CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA	: : : : : : : : : : : : : : : : : : : :	239 239 236 137 -
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa7 LpMDHa1 LpMDHa1 LpMDHa2 LpMDHa3		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300 CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA	: : : : : : : : : : : : : : : : : : : :	239 239 236 137 - - 300 299 299
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa7 LpMDHa1 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa3		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCCAAGGTGAGGCTCCGGGAAGAA	:::::::::::::::::::::::::::::::::::::::	239 239 236 137 - - 300 299 299 299
LpMDHa2 LpMDHa3 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA	:::::::::::::::::::::::::::::::::::::::	239 239 236 137 - 300 299 299 296 197
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa4 LpMDHa5 LpMDHa6		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTTTTTT		239 239 236 137 - 300 299 299 296 197 17
LpMDHa2 LpMDHa3 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA	:::::::::::::::::::::::::::::::::::::::	239 239 236 137 - 300 299 299 296 197
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa4 LpMDHa5 LpMDHa6		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGGAAGAA TGTGCAATCAACTATCACAGGACTGCCATTCTTTTTTTTT		239 239 236 137 - 300 299 299 296 197 17
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa4 LpMDHa5 LpMDHa6		TTTTGGTGATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTTGCCTCCAAGGTGAGCTCCGGAAGAA TGTGCAATCAACTAACAACTACAAAAAAAAAA		239 239 236 137 - 300 299 299 296 197 17
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa4 LpMDHa5 LpMDHa6		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA AA  * 320 * 340 * 360  TGGAGTCGAGGAAGGGAAGGGTTTTGG		239 239 236 137 - 300 299 299 296 197 17
LpMDHa2 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa7 LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa5 LpMDHa6		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA   * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA		239 239 236 137 
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7  LpMDHa1 LpMDHa2 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa5 LpMDHa5 LpMDHa1		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA   * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA		239 239 236 137 
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7  LpMDHa1 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa5 LpMDHa5 LpMDHa6 LpMDHa1 LpMDHa1		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACATATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA		239 239 236 137 
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7  LpMDHa1 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa5 LpMDHa5 LpMDHa6 LpMDHa5 LpMDHa6 LpMDHa6 LpMDHa7		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA  GTNANGCTCGGNNAGAA  AA  * 320 * 340 * 360  TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTTTGGAAGGAA		239 239 236 137 
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7  LpMDHa1 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa5 LpMDHa6 LpMDHa5 LpMDHa6 LpMDHa6 LpMDHa7		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA		239 239 236 137  300 299 299 296 197 17 2 360 359 359 356 257
LpMDHa2 LpMDHa4 LpMDHa5 LpMDHa6 LpMDHa7  LpMDHa1 LpMDHa3 LpMDHa3 LpMDHa4 LpMDHa5 LpMDHa5 LpMDHa5 LpMDHa6 LpMDHa5 LpMDHa6 LpMDHa6 LpMDHa7		TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA  * 260 * 280 * 300  CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA  GTNANGCTCGGNNAGAA  AA  * 320 * 340 * 360  TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTTTGGAAGGAA		239 239 236 137 

LpMDHa1: LpMDHa2: LpMDHa3: LpMDHa4: LpMDHa5: LpMDHa6: LpMDHa6:	* 380 * 400 * 420  AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG	: 420 : 419 : 419 : 416 : 317 : 137
LpMDHa1: LpMDHa2: LpMDHa3: LpMDHa4: LpMDHa5: LpMDHa6: LpMDHa6:	* 440 * 460 * 480  TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTT  TTAATTAATTTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTT  TTAATTAATTTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTGTTT  TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTG  TTGATTAAATTTTGCAGATTATAGCAAATCCAGGTCTAGTTGAGGGGTCTGTTTTTTGACTTT  TTGATTAAAATTTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTTGACTTT  TTGATTAAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTTGACTTT  TTGATTAAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTTGACTTT	: 475 : 474 : 474 : 471 : 377 : 197 : 182
LpMDHa1: LpMDHa2: LpMDHa3: LpMDHa4: LpMDHa5: LpMDHa5: LpMDHa6: LpMDHa7:	* 500 * 520 * 540  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTTACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA  TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA	: 535 : 534 : 534 : 531 : 437 : 257 : 242
LpMDHa1 : LpMDHa2 : LpMDHa3 : LpMDHa4 : LpMDHa5 : LpMDHa6 : LpMDHa7 :	* 560 * 580 * 600  ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG ATMCCNGCGCGCNN- ATCCGGCGGCGTAATGCCACAMAACATTACTTGGACAAGAGGGAACTAGTTCGGGTMAAG ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG	: 595 : 594 : 594 : 544 : 497 : 317 : 302
LpMDHa1 : LpMDHa2 : LpMDHa3 : LpMDHa4 : LpMDHa5 : LpMDHa6 : LpMDHa7 :	* 620 * 640 * 660  TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAA	: 650 : 649 : 649 : - : 557 : 377 : 345
LpMDHa1 : LpMDHa2 : LpMDHa3 : LpMDHa4 : LpMDHa5 : LpMDHa6 : LpMDHa7 :	* 680 *  GTGANTCCATTGCNCTNAAGCCNAAAAAAAA	

## ure 14 Consensus contig nucleotide sequence of LpMDHb

LpMDHb	:	* TTTGGTNCTTT	20 rgccgagcgagaaa	* CTGTTCGG	40 rgtcaccacco	* CTTGNGTTGTT	60 CGTGC :		60
LpMDHb	:	* TAAAACTTTCT!	80 ACGCTGGGAAGGCAA	* \ACGTGCCA(	100 GTCACTGGGG	* TGAATGTTCCT	120 GTTGT :	: :	120
LpMDHb	:	* TGGTGGCCATG	140 CTGGTGTTACTATCC	* CTGCCACAG	160 TTCTCACAGG	* CTACTCCTGCA	180 AGTAA :	: !	180
ГБИДНР	:	* TGCATTGTCCC	200 ATGAGGACCTTAAGO	* BCCCTCACC	220 AAGAGGACAC	* AAGATGGTGGG	240 BACGGA :	:	240
грмонр	:	* AGTTGTTGAAG	260 CAAAGGCTGGAAAGG	* EGCTCAGCA	280 ACATTGTCAA	* TGGCATATGCI	300 GGTGC	:	300
LpMDHb	:	* AGTATTTGGAG.	320 ATGCATGCTTGAAG	* EGGCTCAAT	340 GGAGTTCCTG	* ACATTGTAGAC	360 STGCTC	:	360
LpMDHb	:	* CTTTGTGCAAT	380 CAACCGTAACAGAG(	* CTGCCATTC	400 TTTGCCTCCA	* AGGTAAGGCT(	420 CGGCAA	<b>:</b>	420
LpMDHb	:	* GAACGGAGTGG	440 AGGAAGTGATTGGG	* CTGGGCGAG	460 SCTGTCTGCCT	* TCGAGAAĠGA(	480 GGTCT	:	480
LpMDHb	:	* GGAGAGCCTCA	500 AGGGCGAGCTGNTG	* NCCTCCATO	520 CGAGAAGGGTA	* ATCAAGTTCGC	540 GCAGGA	:	540
LpMDHb	:	* GAGCTAGTCAA	560 CCTGCTCAGATTCT	* AACACTCCG	580 SCACATGAACI	* CCGGTGGGATC	600 IGATGA	:	600
LpMDHb	:	* ATTTTTGGTAC	620 GACTCCTTTCACTG	* CCCCCTTC1	640 CCTGGGGACA	* ATTGAGGCGTC	660 GNGCTC	:	660
LpMDHb	•	* CACAATAAAAT	680 GGCGTGNCTTGTTG	* CCATACTGA	700 AACTGAACTTG	* STAATACCAGA	720 AAGAGT	:	720
гьмонр	•	* GAAACCCTGTG	740 SCCTTATGTACCACA	* GTACGGTG!	760 AACCCGAAAAT	* CATGAAGGTA	780 GCAGAA	:	780
		*	800						

LpMDHb : GATTCTGTGGAAGCTTTTTTTTTTAN : 807

. гъмднр	:	* 20 * LXLLPSEKAVRCHHPXVVRAKTFYAGKANVPVTG	40 VNVPVVGGHA	* GVTILPQFSQATP	60 ASN :	60
LpMDHb	:	* 80 * ALSHEDLKALTKRTQDGGTEVVEAKAGKGSATLS	100 MAYAGAVFGD		120 ÆCS :	120
LpMDHb	:	* 140 * FVQSTVTELPFFASKVRLGKNGVEEVIGLGELSA	160 FEKEGLESLK	* KGELXXSIEKGIKF	180 PAQE :	180
LpMDHb	:	S : 181				

gure 16 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHb

LpMDHb1 LpMDHb2	:	* 20 * 40 * 60  TTTGGTNCTTTTGCCGAG-MANAGCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGCTGCGAGAGAGCTGTTMGGTGTCACCACCCTTGMGTTGTTCGTGCT	:	60 44
LpMDHb1 LpMDHb2	:	* 80 * 100 * 120 AAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGTTG AAAACTTTCTACGCTGGGAAGGCAAACGTGCCGGTCACTGGGGTGAATGTTCCTGTTGTTG		121 105
LpMDHb1 LpMDHb2	:	* 140 * 160 * 180  GTGGCCATGCTGGTGTTACTATCCTGCCACÄGTTCTCACAGGCTACTCCTGCAAGTAATGC GTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC	:	182 166
LpMDHb1 LpMDHb2	:	* 200 * 220 * 240 ATTGTCCCATGAGGAÜCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT ATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT	:	243 227
LpMDHb1 LpMDHb2	:	* 260 * 280 * 300 GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGCAGTAT GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCGATGGCATATGCTGGTGCAGTATT	:	304 288
LpMDHb1 LpMDHb2	:	* 320 * 340 * 360  TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT  TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT	:	365 349
LpMDHb1 LpMDHb2	:	* 380 * 400 * 420  GCAATCAAC∐GTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA GCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA	:	426 410
LpMDHb1 LpMDHb2	:	* 440 * 460 * 480  GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC GTGGAGGAGTGATTGGGCTGGGC	:	487 471
LpMDHb1 LpMDHb2	:	* 500 * 520 * 540  TCAAGGGCGAGCTGHTGHCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC  TCAAGGGCGAGCTGHTGHCCTCCATHGAGAAGGGTATCAAGTTCGCHCAGGAGAGCTAGTC	:	548 532
LpMDHb1 LpMDHb2	:	* 560 * 580 * 600 *  AACCTGCTCAGATTCTĞACACTCCGÇACATGAACTCGGTGGGATCTGATGAATTTTTGGTA  AACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGAATTTTTGGTÜ	:	609 593
LpMDHb1 LpMDHb2		620 * 640 * 660 * CGACTCCTTTCIICTGCCCCEITTIITCETGGGGACATTGAGGCGTEIGNGCTEICACAIITAAAAT CGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGIIGCTCCACAATAAAAT	:	670 654
PbWDHp1	:	680 * 700 * 720 *  GGCGTGNÏTTGTTG-CATACTGANCTGAGCTTNÏTAÏTZÏZ GGCGTGIÏCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGTGAAACCCTGTGC	:	708 715

740 \* 760 \* 780 \*

LpMDHb1: CTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAAGATTCTGTGGAAG: 776

800

LpMDHb1 : ----- : -LpMDHb2 : CTTTTTTCTTTTAN : 790

		*	20	*	40	*	60		
LpMDHc	:	GNNGGTNTACCGAGC	CNCATACTTTNG	TGGGTGAG	GTTCTTGGACTN	GACCCAAG	AGAT	:	60
		•	80	*	·100	*	120		
LpMDHc	:	GTCAATGTTCCTGTNO		 CCGGAGTT		CTCCTTTC		:	120
<b>JP</b> 1.D21.0	٠								
					•				
		*	140	*	160	*	180		
LpMDHc	:	GTTAATCCTCCCTGCT	CATTCACCATGA	GGAAATTA	GTATCTCACCTT	CACAGCAT.	ACAG	:	180
		*	200	*	220	*	240		
LpMDHc	:	AATGGTGGGACAGAA	etngtcgaggcga	<b>AAGCTGGA</b>	GCAGGATCGGNN	ACTNTTTC	TATG	:	240
			260	*	280	*	300		
LpMDHc	:	GCGNATGCGGCAGCT	· · · = -	CTTGCTNG		GGTGATGC		:	300
					•		2.50		
LOMDHO		* ATAGNGGANTGCTCT	320 • איייייייייייייייייייייייייייייייייייי	* እርርጥርአርር	340 Cancontrovers	╸ <del>▼</del> ͲͲͲϾϹϪͲϹ	360		360
LpMDHc	•	ATAGNGGANTGCTCT.	AIGIGGALICIC	AGGIGACG	GANCINICITIN	111GCA1C	CAAA	٠	300
		*	380	*	400	*			
LpMDHc	:	GTTCGCCTTGGTTGTT	CTGGCGTCNAGG	AGATCTTG	CCACTTGGTCCA	CTCAACGA	GTN :	4	119

#### Deduced amino acid sequence of LpMDHc

20 40 60 LpMDHc : XGXPSXHTXVGEVLGXDPRDVNVPXXGGHAGVXILPLLSQVNPPCSFTMRKLVSHLHSIQ : 60

80 100 120

 $\verb|LpMDHc|: \verb|NGGTEXVEAKAGAGSXTXSMAXAAAKFADACXRGLHGDAGIXXCSYVDSQVTXXSXFASK|: 120 \\$ 

· LpMDHc : VRLGCSGVXEILPLGPLNE : 139

		* 20 * 40	* 60		
LpMDHd	:	: GNGNTTCCGCCAACACACACCCCCGCTCCCCGTCCGCATCT	CTCCCTTTCGCCTCCAT	:	60
		•			
			+ 120		
_		* 80 * 100	* 120	_	120
LpMDHd	:	: CGATCCAGATCCCACACACCGCCGCAGCCAGCAACGATGAGGC	CGTCGGCGATGAGATCC	•	120
		•	•		
		* 140 * 160	* 180		•
LaMpud		: GCCGCGCAGCTCCTCCGCCGCCGCAGCTACTCGTCCGCGTCCG		:	180
пришна	•	. GCCGCGCAGCICCICCGCCGCCAGCIACICGCCGCGC		•	
		•			
		* 200 * 220	* 240		
Lomdhd	:	: GTGGCCATCCTCGGCGCGGCGGCGGGATCGGGCAGCCGCTGG	CGCTCCTCATGAAGCTG	:	240
•					
-					
		. * 260 * 280	* 300		
LpMDHd	:	: AACCCGCTCGTCTCCCTCTCCCTCTACGACATCGCCGCCA	ACCCCGGCGTCGCCGCC	:	300
			* 360		
T 1		* 320 * 340			260
трмпна	:	: GACGTCTCCCACATCAACTCCCCGGCCCTGGTGAAGGGGTTCA	TGGGCGACGATCAGCIC	•	300
		* 380 * 400	* 420		
PHUMOLI		: GCGGAGGCGTTGGAGGGGGCCGACCTCGTCATCATCCCGGCCG		:	420
Dpi-Dita	•	. GCGGAGGGTTGGAGGGGGGGGTGGTGGTGGTGGG			
		* 440 * 460	* 480		
LpMDHd	:	: GGCATGACCAGGGACGATCTCTTCAACATCAACGCCGGCATCG	STTAAGAACCTCTGCACC	:	480
_					
		* 500 * 520	* 540		
LpMDHd	:	: GCCATCGCCAAGTACTGCCCCAACGCTCTTATCAACATGATCA	AGCAACCCTGTGAACTCA	:	540
		* 560 * 580	* 600		
LOMDER		: ACTGTTCCAATTGCTGCTGAAGTTTTCAAGAAGGCTGGAACCT		•	600
ppribna	•	: ACIGIICCAMIIGUICIOCACIIIICAACAACCICCAACCI		·	
		* 620 * 640	* 660		
LpMDHd	:	: TTTGGTGTGACCACTCTTGATGTTGTTCGTGCCAGGACTTTCT	TATGCTGGGAAGGCTAAT	:	660
		•			
		* 680 * 700	* 720		
LpMDHd	:	: GTACCTGTTACTGGTGTGAACGTTCCTGTTGTTGGTGGTCATG	CTGGTATCACCATTCTG	:	720
•					
		± 740 ± 770	•		
Twantia	_	* 740 * 760	GTGNAGACATN . 774		•
Phinug	:	: CCACTGTTCTCACAGGCAACTCCTTCGACTAATGCATTGTCTA	AGIGMAGACMIN : //4		

LpMDHd : PLFSQATPSTNALSSEDX : 258

LpMDHd	:	* 20 * 40 * 60 XXPPTQHHRSPVRISPFRLHRSRSHTPPQPATMRPSAMRSAAQLLRRRSYSSASGQPERK	:	60
LpMDHđ	:	* 80 * 100 * 120 VAILGAAGGIGQPLALLMKLNPLVSSLSLYDIAATPGVAADVSHINSPALVKGFMGDDQL	:	120
LpMDHd	:	* 140 * 160 * 180 AEALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKNLCTAIAKYCPNALINMISNPVNS	:	180
LpMDHd	:	* 200 * 220 * 240 TVPIAAEVFKKAGTYDEKKLFGVTTLDVVRARTFYAGKANVPVTGVNVPVVGGHAGITIL	:	240
		*		

### gure 21 Nucleotide sequence of LpMDHe

LpMDHe	:	* TCCGTACNATTGCT	20 GCTGAAGTATT	* TAAAAAAGC	40 rgggacataca	* AATCCTAAGAG	60 ATTGT	:	60
LpMDHe	:	* TGGGGGTGACAACA	80 CTTGATGTAGI	* CGAGAGCCAA	100 TACTTTTGTG	* GGTGAGGTTCT	120 TGGAÇ	:	120
LpMDHe	:	* TTGACCCCAGAGAT	140 GTCAATGTTC	* CTGTTGTTGG	160 CGGGCATGCC	* GGAGTTACGAT	180 ATTAC	:	180
LpMDHe	<b>:</b>	* . CACTCCTTTCGCAG	200 GTTAGTCCTC	* CCTGCTCGTT	220 CACCCCTGAG	* GAAATTAGTTA	240 ATCTCA	:	240
LpMDHe	:	* CCTCACGCATACAG	260 AATGGTGGGA	* CAGAAGTTGT	280 GGAGGCGAAA	* GCAGGAGCAGG	300 ATCGG	:	300
LpMDHe	:	* CAACTCTTTCTATG	320 GCGTATGCGG	* CAGCTAAATT	340 · TGCAGATGCT	* TGCTTGAGAGG	360 SATTGC	:	360
LpMDHe	:	* ATGGTGATGCTGGG	380 ATAGTGGAGT	* GCTCTTATGT	400 GGATTCTCAG	* GTGACCGGAAC	420 CTGCCT	:	420
LpMDHe	:	* TCTTTGCATCCAAA	440 AGTTCGCCTAG	* GTCGTTCTGG	460 CGTCGAGGAG	* ATCTTGCAACT	480 TTGGGT	:	480
LpMDHe	:	* CCACTGAACCAGGI	500 TTTTGAAAGAN	* CTGGACTGGA	520 ANAAGGCGAF	* ANAANGAGCTA	540 ATCCCG	:	540
LpMDHe	:	* AGAGCCTTCCAGAA	5 <sup>.</sup> 60 AAGGNTGTGTC	* ATTTCGTNC#	580 ACAAAGTGAG	* STTACATGCCA	600 CATCT	:	600
LpMDHe	:	* TTGTTGGATGTGCT	620 FTCCCCAAAGT	* TCCAACACAC	640 CCGTCGNAATI	rggcatatana'	660 TATTGC	:	660
LpMDHe	:	* TGGTTTGGGGCCT	680 TTTGCNTTNAT	* GCAAACAGG(	700 CTACCTTNTGO	* GGTGGGGGGG	720 ICCGTT	:	720
LpMDHe	:	NTGAAAAACTCTTA	740 AACATTTTTT	* TTACGGTTG(	760 SNAACAAAATI	* VTNTGAAAAGC	780 CTGAGA	:	780
LpMDHe	:	* ANTATATGATAAN	008 TTDAAAAGTT	* AAAAAANNT'	AAN : 816	•			

LpMDHe	:	* 20 * 40 * 60 RXIAAEVFKKAGTYNPKRLLGVTTLDVVRANTFVGEVLGLDPRDVNVPVVGGHAGVTILP .	:	60
LpMDHe	:	* 80 * 100 * 120 LLSQVSPPCSFTPEBISYLTSRIQNGGTEVVEAKAGAGSATLSMAYAAAKFADACLRGLH	:	120
Грирне	:	* 140 * 160 * 180 GDAGIVECSYVDSQVTGTAFFASKVRLGRSGVEEILQLGSTEPGFERXGLEXGEXXSYPE	:	180
LpMDHe	:	* 200 * 220 * 240 SLPERXCHFXQQSELHAIIFVGCASPKFQHTVXIGIXILLVWGLLXXCKQATXWVGGVRX	:	240
LpMDHe	:	* 260 * EKLLTFFFTVXNKXXEKPEXYMIXEXSXXKK : 271		

### ure 23 Consensus contig nucleotide sequence of LpMDHf

LpMDHf	:	* 20 * 40 * 60  GGGATGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC	:	60
LpMDHf	:	* 80 * 100 * 120 AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC	:	120
LpMDHf	:	* 140 * 160 * 180 ATTGCGGCAGAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG	:	180
LpMDHf	:	* 200 * 220 * 240 ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGNTGATCCT	:	240
LpMDHf	:	* 260 * 280 * 300 AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG	:	300
LpMDHf	:	* 320 * 340 * 360  NCCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC	:	360
LpMDHf	:	* 380 * 400 * 420 ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG	:	<b>420</b>
LpMDHf	:	* 440 * 460 * 480 TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT	:	480
LpMDHf	:	* 500 * 520 * 540 GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA	:	540
LpMDHf	:	* 560 * 580 * 600 ACAAAAGTGAGGTTAGGTCGTGGCGAGCTGAGGAGATCCTCCCTC	:	600
LpMDHf	:	* 620 * 640 * 660 GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG	:	660
LpMDHf	:	* 680 * 700 * 720 GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGG	:	720
LpMDHf	:	* 740 * 760 * 780 ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT	:	780
LoMDHf	:	* CTCTCCTGCCTGTAAGAA : 798		

LpMDHf : CTCTCCTGCCTGTAAGAA : 798

## gure 24 Deduced amino acid sequence of LpMDHf

LpMDHf	:		20 * AIVNLISNPVNS	40 rvpiaaexfki	* 60 RAGTYCPKRLLGVTTLDVAR	:	60
LpMDHf	:	* ANTFVAEVLGXDPREXSV	80 * PXVGGHAGITIL	100 PLLXQVSPPC	* 120 SFTPDEISYLTNRIQNGGTE	:	120
LpMDHf	:		40 * AAKFADACLRGM	160 RGDAGIVECX	* 180 YVASEVTELPFFATKVRLGR	:	180
LpMDHf	:	* 2 GGAEEILPLGPLNDFERA	00 * GLEKAXKELSES	220 IQKGVAFMNK	: 220		

gure 25 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHf

LpMDHf1 LpMDHf2	:	* GÄÄÄTGATTNATNCA -GGATGATTÄÄTÄCA	20 ACAAAAATGCTGG ACAAAAATGCTGG	* EGCATTGTC EG <mark>-</mark> ATTGTC	40 CGATCAATCTG	* 60 TGAGGGCGTTGCC TGAGGGCGTTGCC	:	60 58
LpMDHf1 LpMDHf2	:	* AAGAGCTGTCCTAAT AAGAGCTGTCCTAAT	80 GCAATAGTGAATT GCAATAGTGAATT	* FTGATCAGO	100 PACCCTGTGAA PACCCTGTGAA	* 120 CTCAACTGTCCCC CTCAACTGTCCCC	:	120 118
LpMDHf1 LpMDHf2	:	* ATTGCGGCAŬAAGNT ATTGCGGCAGAAGÑT	140 TTCAAGAGGGCTC	* GGAACTTAC	160 CTGCCCAAACG	* 180 TCTCCTTGGAGTG TCTCCTTGGAGTG	:	180 178
LpMDHf1 LpMDHf2	:	ACAACTCTTGATGTA ACAACTCTTGATGTA	200 GCGAGGGCTAACA GCGAGGGCTAACA	* ACCTTTGT( ACCTTTGT(	220 GCTGAAGTGCT GCTGAAGTGCT	* 240 TGNAGNTGATCCT TGGAGÄTGATCCT	:	240 238
LpMDHf1 LpMDHf2	:	* AGAGAAGNCAGTGTT AGAGAAG∏CAGTGTT	260 CCGGNTGTTGGCCCCGG	* GGCATGC EGGCATGC	<b>280</b> ÿGGGATCACTAT AGGGATCACTAT	* 300 ATTGCCCCTCCTG ATTGCCCCTCCTG	:	300 298
LpMDHf1 LpMDHf2	:	* NCCCAGGTCAGCCCC GCCCAGGTCAGCCCC	320 CCGTGCTCATTC CCGTGCTCATTC	* ACTCCAGA' ACTCCAGA'	340 FGAAATCAGCTA FGAAATCAGCTA	* 360 TTTGACTAACCGC	:	360 358 <sub>.</sub>
LpMDHf1 LpMDHf2	:	ATACAGAATGGCGGT ATACAGAATGGCGGT	380 ACCGAAGTTGTT ACCGAAGTTGTT	* GAGGCAAA( GAGGCAAA(	400 GCTGGAGCAGO	* 420 CTCTGCAACTTTG	:	420 418
LpMDHf1 LpMDHf2	:	* TCAATGGCTTTTGCT TCAATGGCTTTTGCT	440 GCTGCAAAATTC	* GCCGATGC GCCGATGC	460 ATGCTTGCGTGC ATGCTTGCGTGC	* 480 AATGCGTGGTGAT AATGCGTGGTGAT	:	480 478
LpMDHf1 LpMDHf2	:	* GCTGGCATTGTGGAA GCTGGÑATTGTGGAA	500 TGTÄCATACGTT TGTN	GCATCTGA	520 GGTGACAGAGC	* 540 GCCGTTCTTTGCA	:	540 497
LpMDHf1 LpMDHf2	:	* ACAAAAGTGAGGTTA	560 AGGTCGTGGCGGA	* GCTGAGGA	580 GATCCTCCCTC	* 600 TTGGGCCACTGAAT	:	600 -
LpMDHf1 LpMDHf2		¢ GACTTTGAGAGAGCT	620 TGGCCTGGAGAAG	* GCGAANAA	640 GGAGCTCAGCG	* 660 AGAGCATCCAGAAG	:	660 -
LpMDHf1 LpMDHf2	:	* GGTGTGGCGTTCATO	680 SAACAAGTGAGAT			* 720	:	720 -

LpMDHf1 : CTCTCCTGCCTGTAAGAA : 798
LpMDHf2 : ----- : -

		· *	20	*	40	*	60		
Lownha		CAATTGCACGTTCTT	GCTCACTTC	AGCATCACCCT	CACGCTTCT	CCTACACAACCC	CTCC	:	60
oprong	•	GB1110G10G11-1-1							
							•		
		*	80	*	100	*	120		
pHQMqJ	:	CAACCGTCACTATGG	TCAAGGCTG	TCGTCGCAGGT	GCTGCTGGT	rggtatcggccag	CCCC	:	120
		*	140	*	160	*	180	_	300
LpMDHg	:	TCTCTCTTCTACTCA	AGACGAGCC	CCCTCATCGAT	GAGCTTGC	CTCTACGATGTT	GTCA	:	180
					220	•	240		
		*	200			CCCTCD D DTCGCC		:	240
LpMDHg	:	ACACTCCCGGTGTTG	CCGCTGATC	"I"I"I'CCCACATC	.1CAICCCG	CGCICAMAICCCC		•	
		•	260	*	280	*	300		
LaMbua		ACCTCCCCAAGGATG	ZOU LATEGEGEAL	AGGCTGCATTC		CGACATTATCGTC	CATCC	:	300
nfumuð	•	ACCICCCAAGGAIG	A1666661	2.000200					
				•					
		*	320	*	340	*	360		
LpMDHa	•	CCGCCGGCATTCCTC	GCAAGCCTG	GCATGACCCGT	GATGACCT	CTTCAACATCAAC	CGCCG	:	360
J	Ī				•				
						•	455		
		*	380	*	400	*	420		420
LpMDHg	:	GAATTGTCAAGGGTC	CTGATTGAGG	STTGCCGCCGA/	AGTTGCCCC	CAAGGCCTTCAT	reree	:	420
					•				
		a.	440	•	460	*	480		
		TCATCTCCAACCCTC	440	· ‹ CCCጥCCጥልጥ	ውያ <del>፤</del> ሚያጋጋንምንም	GGTCCTCAAGGC		:	480
грипна	:	TUATUTUUAAUUUT	SICAMCICIA	ACCOTCCIAL.	01010000.				
		*	500	*	520	*	540		
LpMDHa	:	GCGTCTTCAACCCTC	CAGCGTCTT	TCGGTGTCAC	CACCCTCGA	CATCGTCCGTGC	CGAGA	:	540
-F5	•								
•		*	560	*	580	*	600		
LpMDHg	:	CTTTCGTCGCCAGC	ATCACCGGC	GAGAAGCAGCC	CCAGAACTI	GACCGTCCCCGT	CATTG	:	600
					640	•	660		
		*	620	*	640	יי יי			660
LpMDHg	:	GCGGCCACTCCGGC	GAGACCATC(	GTCCCGCTTTT	CAGCAAGGN	ILCHGCCCICIGC	T 11100	•	550

LpMDHg : TTCCCGC : 667

\* 20 \* 40 \* 60

LpMDHg : IARSCSLQHHPHASPTQPLPTVTMVKAVVAGAAGGIGQPLSLLLKTSPLIDELALYDVVN : 60

LpMDHg : TPGVAADLSHISSRAQIAGYLPKDDGAKAAFKDADIIVIPAGIPRKPGMTRDDLFNINAG : 120

LpMDHg : IVKGLIEVAAEVAPKAFILVISNPVNSTVPISAEVLKAKGVFNPQRLFGVTTLDIVRAET : 180

LpMDHg : FVASITGEKQPQNLTVPVIGGHSGETIVPLFSKXQPSAXIP : 221

LpMDHh	:	* TNACGGAGCTGCTTAAA	20 TCAGCCCCCAT	* rccgcctcg	40 TCȚATAGCGAT	* CCTTCATCC	60 CGT :		60
LpMDHh	:	* TGTCGTCGCCTCCTCCC	80 GAACCACTCTC		100 GAACTCCAGAA		L20 ATG :	1	120
LpMDHh	:	* GCGGCGAAGGAACCGAT	140 GCGCGTGCTCG		160 CCGCAGGACAA		180 GCT :		180
LpMDHh	:	* CTTGTTCCGATGATTGC	200 TAGGGGAATTA		220 CGGACCAGCCT		240 CAT :	:	240
LpMDHh	:	* ATGCTGGATATTCCACC	260 CAGCTGCTGAAG	* CTCTTAATG	280 GTGTTAAGATG		300 GAT :	:	300
LpMDHh	:	* GCCGCATTTCCACTTC	CAAGGGÄGTTG	* TTGCAACAA	340 ACTGATGTTGTT		360 ACT :		360
LpMDHh	:	* GGTGTGAATGTTGCGG	380 PTATGGTTGGTG	* GATTCCCC#	400 AGGAAGGAGGGA		420 AAG :		420
LpMDHh	:	* GATGTTATGTCTAAGA	440 ATGTTTCAATCI	* 'ACAAATCT(	460 CAAGCATCTGC		480 CAT :		480
LpMDHh	:	* GCAGCÇCCGAATTGCA	500 AGGTTCTGGTTC	* FTTGCCAAT(	520 CCAGCAAACAC	* CAATGCTCTI	540 ATC :		540
LpMDHh	. :	* TTAAAGGAGTTTGCTC	560 CATCTATTCCT(	* BAGAAGAAC	580 ATCAGTTGTTT	* GACCCGCCTA	600 \GAC :		600
LpMDHh	. :	* CATAACAGGGCACTTG	620 GTCAGATCTCTC	* BAGAGACTT	640 Gatgtccaagt	* TAGTGATGT	660 SAAG :		660
LpMDHh	ı :	* AATGTTATCATCTGGG	680 GCAATCACTCT	* rccagtcag	700 TACCCTGATGT	* GAACCACGC(	720 CACC :	;	720
LpMDHh	1 :	* GTGAAGACTTCCAGTG	740 GCGAGAAGCCT	* GTTCGCGAA	760 CTTGTTAAAGA	* CGATGAATGO	780 GCTA :	:	780
LPMDH	1	* AATGCAGGGTTCATTG	800 CCACTGTCCAG	* CAGCGTGGT	820 GCTGCAATCAT	* CAAAGCGAG(	840 Saag	•	840
LpMDHl	ı	* CTCTCCAGTGCTCTCT	860 CCTGCTGCCAGC	* TCTGCTTGT	880 GACCACATCCG	* TGATTGGGT	900 PCTC	:	900
LpMDHl	a	* : GGAACCCCTGAGGGAI	920 ACATTTGTTTCC	* ATGGGTGTG	940 TATTCTGATGG	* TTCATACGG	960 TGTG	:	960

1000 980 LpMDHh : CCTGCTGGGCTTATCTACTCCTTCCCAGTAACTTGCTGCGGTGGAATGGACAATTGTT : 1020 1060 1040 1100 \* 1120 LPMDHh : TCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAGTAACTGCATACCAGGGAGCAGCTG : 1140 1180 1200 1160 LpMDHh : CCGCTCTGATGTTTTGAATAAAGGAACATTTTGGCTCCATGAAACTCATCTCCACTCAG : 1200 1240 1260 1220 1280 \* 1300 LpMDHh : GTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTGGCAGGAAGATTGGAACAA : 1320 1340 \* 1360 1400 \* 1420 LpMDHh : AGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGAGGATTGGAACAATT : 1440

 LpMDHh : VQGLPIDEFSRKKMDATAQELSEEKALAYSCLE : 333

LpMDHh : MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEALNGVKMELV : 60 LpMDHh : DAAFPLLKGVVATTDVVEACTGVNVAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEA : 120 LpMDHh : HAAPNCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLDVQVSDV : 180 Lpmdhh : KnviiwgnhsssqypdvnhatvktssgekpvrelvkddewlnagfiatvQQrgaAiikar : 240 LpMDHh : KLSSALSAASSACDHIRDWVLGTPEGTFVSMGVYSDGSYGVPAGLIYSFPVTCCGGEWTI : 300 

rigure 30 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHh

		* 40 * 60		
		* 20 * 40 * 60  TNACGGAGCTGCTTAAATCAGCCCCCATTCCGCCTCGTCT_C_ACHATCCTTCATCCCGTTG	:	60
LpMDHhl :	:		:	29
LpMDHh2	:		:	24
LpMDHh3	:	- ETATAGCGTTNCTAC - CNNTGTN	:	22
LpMDHh4	:		:	20
LpMDHh5	:		:	19
LpMDHh6	:		:	18
LpMDHh7	:	GC PATCCTTCATCCCGTTG		19
LpMDHh8	:		:	19
LpMDHh9	:	OCARTOCITO NIA BETT TO A TOTAL OCCUPANTO CANCECCO TO TOTAL OCCUPANTO CANCECCO TO TOTAL OCCUPANTO CANCECCO TO TOTAL OCCUPANTO CONTROL OCCUPANTO CANCECCO TO TOTAL OCCUPANTO CANCECCO CANCECCO TOTAL OCCUPANTO CANCECCO TOTAL OCCUPANTO CANCECCO CANCECCO TOTAL OCCUPANTO CANCECCO CONTROL OCCUP	:	18
LpMDHh10	:		:	18
LpMDHh11	:		•	17
LpMDHh12	:		•	16
LpMDHh13	:	GATCCTT ATCCCGTTG  GNNACCTTGTCCCGTTG	•	17
LpMDHh14	:		•	17
LpMDHh15	:	GATCCTTCATCCCGTTG	:	
LpMDHh16	:	GNTCCTTCATCCCGTTG	:	17
LpMDHh17	:	GATCCTT ATCCCGTTG.	:	16
LpMDHh18	:	GÑŢĊĊĠŢĊĂŢĊĊĠŢŢĠ	:	17
LpMDHh19	:	GNNCCTTCATCCCGTTG	:	17
LpMDHh20	:	GMTCCTT-NTCCCGTTG	:	16
LpMDHh21	:	GWTCCTTCATCCCGTTG	:	17
LpMDHh22	:	GATCCTTCATCCCGTTG	:	17
LpMDHh23	:	GÑCCTTŴATCCCÑTTG	:	16
LpMDHh24	:	GWICGTINATCCCGTTG	:	16
LpMDHh25	:	ŢŢĊŢŢŊĊŢĊĊĠŢŢĠ	:	16
LpMDHh26	:	TCCTTWATCCCGTTG	:	15
LpMDHh27		ACCTTC NCCCGTTG	:	15
LpMDHh28		TCCTT-NTCCCGTTG	:	14
LpMDHh29	:	TCCTT-ATCCCGTTG	:	14
LpMDHh30	:	TCCTTCNTCCCGTTG	:	15
LoMDHh31	:	CCTTCATCCCGTTG	:	14
LpMDHh32	:	NCGTFGTCCCNTTG	:	14
LpMDHh34	•	ACCTLATCCCGTTG	:	14
LpMDHh35		CTTÄCTCCCGTTG	:	13
LpMDHh36	•	TTNC NCCGNCTG	:	13
LpMDHh37	•	TINC MACCOCCAG	:	13
LpMDHh38	•	ŢŢŢĊŢŢĊĊŢŢĠ	:	13
LpMDHh39	•	-TTCATCCCÑTTG	:	12
LpMDHh40	•	TTGATCCCGTTG	:	12
	•	Triatcccgetg	:	12
LpMDHh41	•	STUATECCETTC	:	12
LpMDHh42	1	- ctcnrcccttc	:	12
LpMDHh43	•	MICCOGUIG	:	11
LpMDHh44	•	TITOTCCCGTTC	:	11
LpMDHh45		тій тесестте	:	11
LpMDHh46	•	TCCCGTTC	:	8
LpMDHh47	•	c <u>e</u> -trg	:	5
LpMDHh48			:	6
			:	_
LpMDHh50			:	_
LpMDHh51		***************************************	:	_
LpMDHh52			:	_
LpMDHh53			•	_
LpMDHh54			•	
LpMDHh55			•	_
LpMDHh56			•	_
LpMDHh57			:	_
LpMDHh58				_
LpMDHh59				_
LpMDHh60		*		-
LpMDHh61			:	_
LpMDHh62			:	-
LpMDHh63			:	-
LpMDHh64			:	-

120 100 80 CGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 122 LpMDHh1 T<mark>-G-CTNCTECECEN-</mark>AACCACTCTCCCCANCCCCGAACTCCAGAACCGGCTCCAATGGCGG 88 LpMDHh2 86 TCGCCTCCTCCCGA©CCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh3 83 TCGCCTCCTCCCG-AAAACNCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh4 TCGTCGCCTCCTCCGAACCACTCTNCCCNNCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh5 80 TCGTCGCCTCCTCCCGAMCCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh6 TCG-CHMCTCCTCCC-GACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGCCGG 78 LpMDHh7 81 TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh8 TCGTCGCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 81 LpMDHh9 79 TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh10 80 TCGTCACTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh11 TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 LpMDHh12 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 77 TCGTCGCCTCCTCCCG LpMDHh13 TCGTCGCCTCCTCCCGĂACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 LpMDHh14 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 TCGTCGCCTCCTCCCG LpMDHh15 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 TCGTCGCCTCCTCCCG LpMDHh16 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 77 TCGTCGCCTCCTCCCG LpMDHh17 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 **FCGTCGCCTCCTCCCG** LpMDHh18 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 78 LpMDHh19 TCGTCGCCTCCTCCCG 77 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh20 TCGTCGCCTCCTCCCG 78 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG TCGTCGCCTCCTCCCG LpMDHh21 78 ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG TCGTCGCCTCCTCCCG LpMDHh22 ACCACTCTCCCCATCCCGAACTCCAGAACCGGCTCCAATGGCGG 77 TCGTCGCCTCCTCCCG LpMDHh23 TCGTCGNCTNCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 77 LpMDHh24 TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG 77 LpMDHh25 TCGTCGCCTCCTCCCGAACC<mark>-</mark>CTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 76 LpMDHh26 TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh27 TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 75 LpMDHh28 TCGTCGCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGCCGG 75 LpMDHh29 TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 76 LpMDHh30 TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 75 LpMDHh31 TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 76 LpMDHh32 TCGTCGCCTCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAACGGCGG 75 LpMDHh34 TCGTCGCCTCCTCCCGAACCACTCTCCCCTTTCCCCGAACTCCAGAACCGGCTCCAATGGCGG TCGTCGCCTCCCCGAACCACTCTCCCCTTCCCCGAACTCCA<mark>-</mark>AACCGGCTCCAATGGCGG 75 LpMDHh35 74 LpMDHh36 TCGTCGCCTCCTCCCGAACCACTCTCCCCMCCCCGAACTCCAGAACCGGCTCCAATGGCGG 75 LpMDHh37 TCGTCGCCTCCTCCG-AÃCÃCTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 74 LpMDHh38 74 TCGTÑGCCTÑCTCCCGÂACCACTCTCCCCÏITCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh39 TCGTCGCCTCCCG\_AACCCCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 73 LpMDHh40 TCGTCGCCTCCCGAACTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 73 LpMDHh41 TCGTCGCCTCCTCCCGAACC<mark>-</mark>CTCTCCCCATCCCCGAACTCC-GAACCGGCTCCAATGGCGG 72 LpMDHh42 TCGTCGCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 73 LpMDHh43 TCGTCGCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 72 LpMDHh44 TCGTCGCCTCCTCCCG\_ACCACTCTCCCC\_TCCCCGAACTCCAGAACCGGCTCCAATGGCGG 71 LpMDHh45: TCGTCGCCTCCTCCCGAACCACTCTCCCC\_TCCCCGAACTCCAGAACCGGCTCCAATGGCGG 72 LpMDHh46: TCGTCGCCTCCCG-ACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG 69 LpMDHh47 TCGTCGCCTCCCG-ACCCTNCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG 65 LpMDHh48 : 68 TCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG LpMDHh49 ------GGACC-CTCTCCCCATCCCCGAACTCCAGNACCGGCTCCAATGGCGG 46 LpMDHh50 -----NCCCCGNANTCCA-NACCGGCTCCAA-GGCGG 30 LpMDHh51 LpMDHh52 LpMDHh53 LpMDHh54 LpMDHh55 LpMDHh56: LpMDHh57 LpMDHh58 LpMDHh59 LpMDHh60 : LpMDHh61 : LoMDHh62 LpMDHh63 LpMDHh64

160 180 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT 184 LpMDHh1 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGAAACAAATTGGATATGCTCTTGTT 150 LpMDHh2 148 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh3 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 145 LpMDHh4 CGAAGÑAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCT<u>T</u>GTT 144 LpMDHh5 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 142 LpMDHh6 140 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh7 143 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh8 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGACAAATTGGATATGCTCTTGTT 143 LpMDHh9 141 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh10 142 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh11 : 140 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh12 139 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh13 : 140 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh14 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh15 : 140 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh16 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh17 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh18: CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh19 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh20 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh21 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 140 LpMDHh22 : CEAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh23 : NGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 139 LpMDHh24 : 139 CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh25 138 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh26: 139 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh27 137 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGACAAATTGGATATGCTCTTGTT LpMDHh28 137 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh29 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 138 LpMDHh30 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh31 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAÑATTGGATATGCTCTTGTT : 138 LpMDHh32 : 137 CÑAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh34 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 137 LpMDHh35 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 136 LpMDHh36 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137 LpMDHh37 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136 LpMDHh38 136 CGAAGGAACCGATGCGCGTGCTCÑTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh39 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT 135 LpMDHh40 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh41 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh42 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135 LpMDHh43 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134 LpMDHh44 : 133 CGAAGGAACCGATGCGCGTGCTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh45 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGACAAATTGGATATGCTCTTGTT : 134 LpMDHh46 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131 LpMDHh47 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127 LpMDHh48 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130 LpMDHh49 108 CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh50 91 CGAAGNAACCGA-GCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT LpMDHh51 --GGACCGATGCCCGTCGTCACCGGCGCCCGCAGGNCAAATTGGATATGCTCTTGTT 57 LpMDHh52 LpMDHh53 LpMDHh54 LpMDHh55 LpMDHh56 LoMDHh57 LpMDHh58 LoMDHh59 LpMDHh60 LpMDHh61 : -LpMDHh62: LpMDHh63 LpMDHh64:

240 200 220 CGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 246 LpMDHh1 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 212 LpMDHh2 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA CCGATGATTGCTAGGCMAATTATGCTTGGNGTGGACMAGCCTGTTATTNTGCATATC CCGATGATTGCTAGGGGAATTATGCTTGGTGUGGACCAGCCTGTTATTCTGCATATGCTGGA 210 LpMDHh3 202 LpMDHh4 206 LpMDHh5 204 LpMDHh6 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 202 LpMDHh7 205 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA LpMDHh8 205 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA LpMDHh9 : 203 LpMDHh10 : 204 LpMDHh11 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 202 LpMDHh12 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 201 LpMDHh13 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 202 LpMDHh14 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 202 LpMDHh15 202 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA LpMDHh16 201  ${\tt CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA}$ LpMDHh17 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 202 LpMDHh18: 202 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA LpMDHh19 201 LpMDHh20 : 202 LpMDHh21 : 202 LpMDHh22:  ${\tt CCGATGATTGCTA} {
m \widetilde{N}} {\tt GGGGAATTATGCTT} {\tt GGTGCGGA} {\tt CCAGCCTGTTATTCTGCATATGCTGGA}$ 201 LpMDHh23: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 201 LpMDHh24: 201 LpMDHh25: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 200 LpMDHh26:  ${\tt CCGATGATTGCTAGGGGGAATTATGCTT}{\tt GGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA}$ 201 LpMDHh27: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh28: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh29: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 200 LpMDHh30 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh31 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 200 LpMDHh32 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh34 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh35 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 198 LpMDHh36: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 199 LpMDHh37 198 CCGATGATTGCTAGGGGAATTATGCTĞGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA LpMDHh38 : CCGATGATTGCTAÑGGGAATTATGCTTGGTGCGGACCAÑCCTGTTATTCTGCATATGCTGGA 19B LpMDHh39: 197 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCAGGA LpMDHh40: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCCGTTATTCTGCATATGCTGGA 197 LpMDHh41 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196 LpMDHh42: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 197 LpMDHh43 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 196 LpMDHh44: CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 195 LpMDHh45 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196 LpMDHh46 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 193 LpMDHh47 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 189 LpMDHh48 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 192 LpMDHh49 CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 170 LpMDHh50 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 153 LpMDHh51 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA 119 LpMDHh52: TATGCTTGGTGCGG-CCAGCCTGTTATTCTGCATATGCTGGA LpMDHh53 LpMDHh54 LpMDHh55 LpMDHh56 : LpMDHh57 LpMDHh58 LpMDHh59 LpMDHh60 : LpMDHh61: LpMDHh62 LpMDHh63 LpMDHh64

260 308 LpMDHh1 274 LpMDHh2 TATTĞCACCAGCTGCTGAAGCTCTTAATGGÜGTTAAĞATGGAÄĞTGNNT-NĞGCĞGCNTÄĞN 271 LpMDHh3 LpMDHh4 268 LpMDHh5 266 LpMDHh6 264 LpMDHh7 267 LpMDHh8 : 267 LpMDHh9 TATTCCACCAGC@GCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC 265 LpMDHh10 : 266 LpMDHh11 264 LpMDHh12 : 263 LpMDHh13 264 LpMDHh14 264 LpMDHh15 264 LpMDHh16 263 LpMDHh17 264 LpMDHh18 264 LpMDHh19 263 LpMDHh20 264 LpMDHh21 TATTCCACCAGCTGCTGAAÏJCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC 264 LpMDHh22 263 LpMDHh23: 263 LpMDHh24: 263 LpMDHh25: 262 LpMDHh26 263 LpMDHh27 261 LpMDHh28 261 LpMDHh29 262 LpMDHh30 261 LpMDHh31 262 LpMDHh32 261 LpMDHh34 261 LpMDHh35 260 LpMDHh36 261 LpMDHh37 260 LpMDHh38 260 LpMDHh39 TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGÑTGATGCCGCATTTC 259 LpMDHh40 259 LpMDHh41 258 LpMDHh42: 259 LpMDHh43: LpMDHh44: 257 LpMDHh45 : 258 LpMDHh46 255 LpMDHh47 251 LpMDHh48 254 TATTCCACCAGCTGCTGAAGCTCTTAATGGTĢTTAAGATGGAGTTGGTTGATGCCGCATTTC LpMDHh49 : 232 LpMDHh50 215 LpMDHh51 181 LpMDHh52 LpMDHh53 LpMDHh54 LpMDHh55 LpMDHh56 LpMDHh57 LpMDHh58 LpMDHh59 LpMDHh60 LpMDHh61 LpMDHh62 LpMDHh63 LpMDHh64:

280

360 340 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 320 CACTT THAN AGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGNGNGAATGT LpMDHh1 NCTTTNTCGCN

: 370

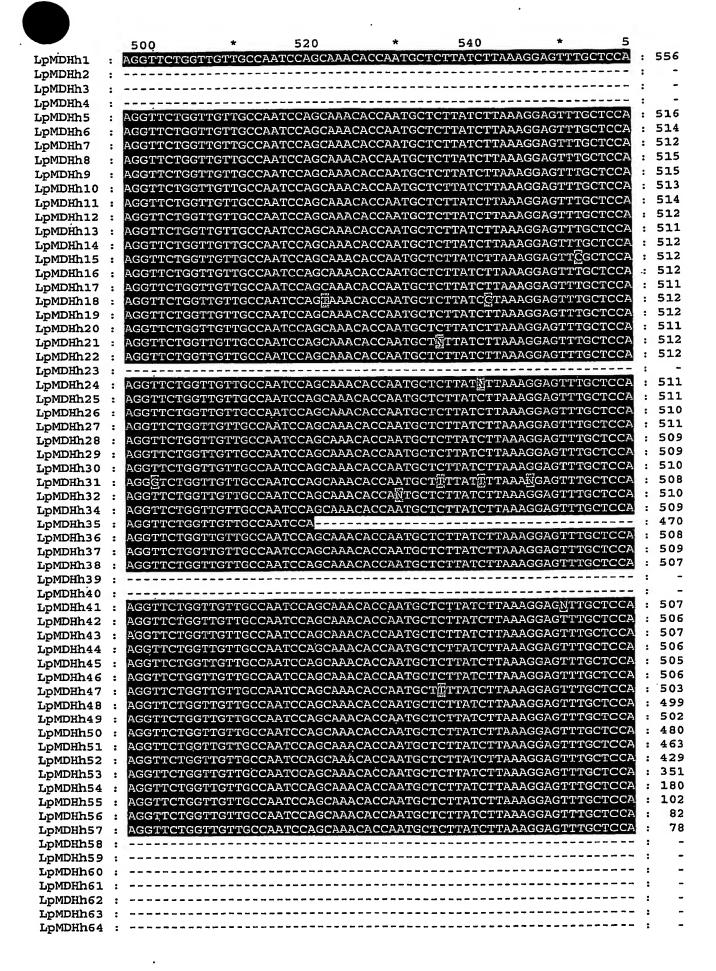
LpMDHh2 282 LpMDHh3 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh4 330 LpMDHh5 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328 LpMDHh6 CACTTCTCAAGGGAGTTGTTGCAACAACTGACGTTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LpMDHh7  $\mathtt{CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT}$ : 329 LpMDHh8 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329 LpMDHh9 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 327 LpMDHh10 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328 LpMDHh11 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 326 LoMDHh12 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325 LpMDHh13 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LoMDHh14 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LpMDHh15 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LpMDHh16 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325 LpMDHh17 CACTTCTCAAGGGAGTTGTTGCGACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 LpMDHh18 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT . 326 LpMDHh19 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325 LpMDHh20 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTAATGTT LpMDHh21: LpMDHh22: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTÄÄGGCTTGCACTGG-----315 CACTTMTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh23: 325 LpMDHh24: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMDHh25 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 324 LpMDHh26: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 325 LpMDHh27: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 323 LpMDHh28: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT . 323 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh29: : 324 LpMDHh30: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323 LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324 LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh34: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323 LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 LpMDHh36: cacttctcaagggagttgttgcaacaactgatgttgttgaggcttgcactggtgtgaatgce : 323 LpMDHh37 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322 САСТТСТСААGGGAGЙТGЙТGCAACAACTGATGTŢGЙTGAGGCTЙGCACTGGŢGTGAATGTT LpMDHh38 : 322 LpMDHh39 CACTTNTCAAGGGAGTTGNTGCAACAACTGATGTNGTTGANGCTTGCACTGGNGTGAATGTT : 321 LpMDHh40 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh41 : : 320 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT LpMDHh42 : 321 LpMDHh43 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh44 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 319 LpMDHh45 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 320 LpMDHh46 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 317 LpMDHh47 CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 313 LpMDHh48: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 316 LpMDHh49: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGITGAGGCTTGCACTGGTGTGAATGTT 294 LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 277 LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 243 LpMDHh52: CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT 165 LpMDHh53 : LpMDHh54 : LpMDHh55: LpMDHh56 LpMDHh57: LpMDHh58 LpMDHh59 : LpMDHh60 : LpMDHh61 : LpMDHh62: LoMDHh63:

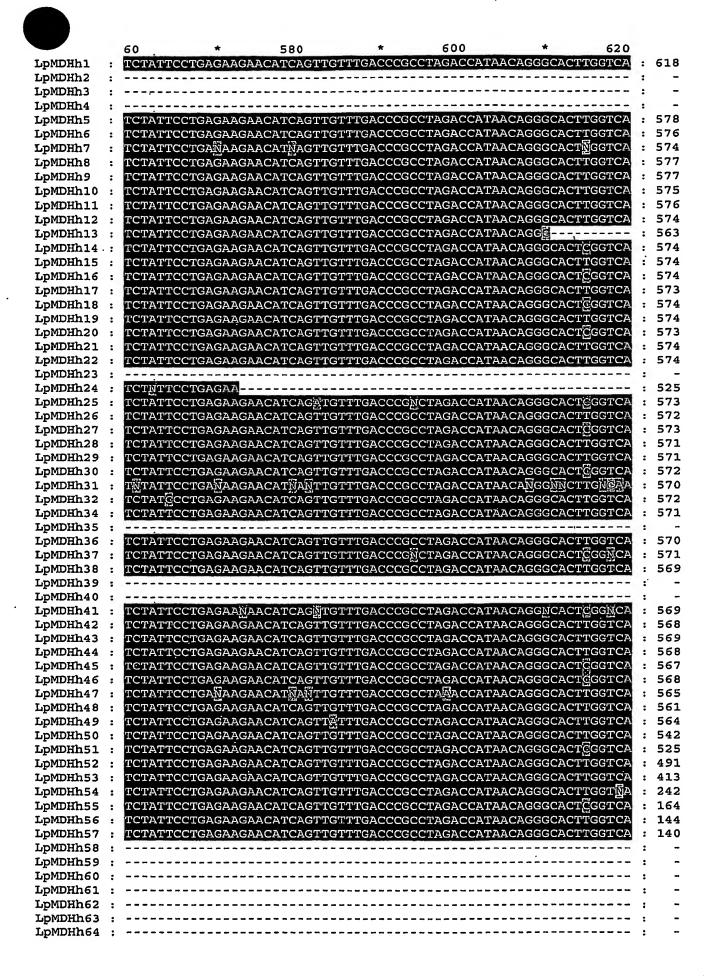
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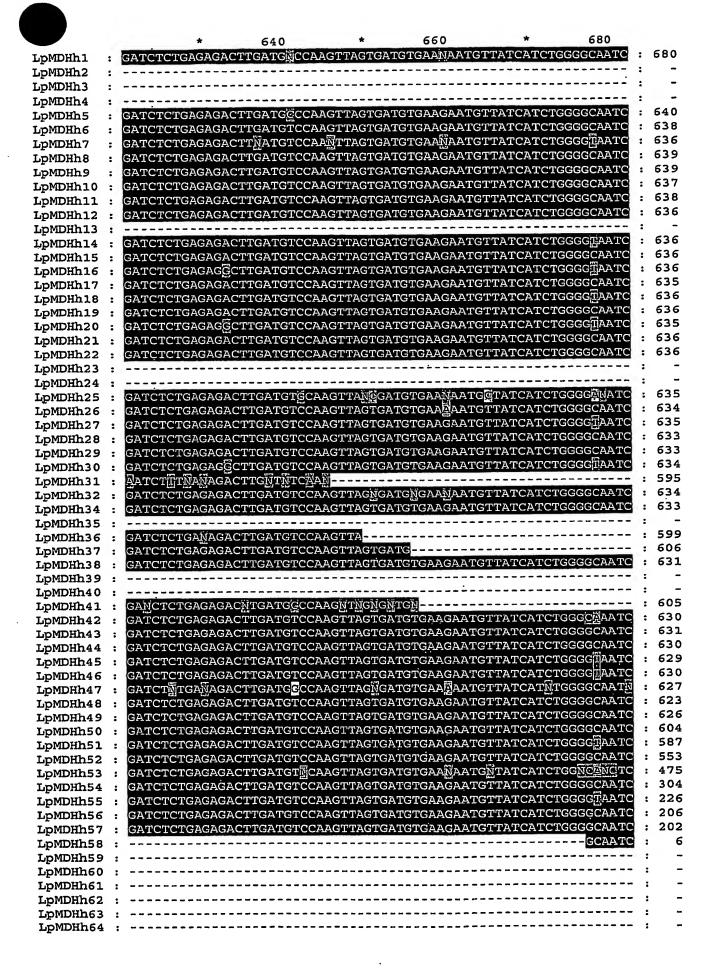
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480 460 440 GAAŢGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA LpMDHh1 LpMDHh2 LpMDHh3 LpMDHh4 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA LpMDHh5 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA LpMDHh6 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCÑAATTGCA : 450 LpMDHh7 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 453 LpMDHh8 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 453 LpMDHh9 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 451 LpMDHh10 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 452 LpMDHh11 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LpMDHh12: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh13 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LpMDHh14: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LpMDHh15 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LpMDHh16 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh17: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LpMDHh18: gaatgtttcaatctacaaatctcaagcatc<u>ë</u>gcccttgaagcccatgcagcccgaattgca 450 LpMDHh19 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh20 GAATGTTTCAATCTACAAATCTCAAGCATCEGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 LoMDHh21 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 450 : LpMDHh22 LpMDHh23 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh24 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh25 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 448 LpMDHh26: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 449 LpMDHh27 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 447 LpMDHh28: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 447 LpMDHh29: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 448 LpMDHh30 : ÇAATGTTTCAATCTACAAATCTEAAGCATCTGCCCTTGAAGCCCATGCA CCCCAAATTGCA 446 LpMDHh31 : AATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 448 LpMDHh32: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 447 LpMDHh34 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA LpMDHh35 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 446 LpMDHh36 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 447 LpMDHh37: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCATGCAGCCCCGAATTGCA 445 LpMDHh38 : LpMDHh39: LpMDHh40 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 445 LpMDHh41: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 444 LpMDHh42: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 445 LpMDHh43: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 444 LpMDHh44: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 443 LpMDHh45 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 444 LpMDHh46 : MAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA GAATGTTTCAATCTACAAATCTCAAGATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 441 LoMDHh47 437 LpMDHh48 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 440 LpMDHh49: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 418 LpMDHh50: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTG[]A 401 GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA LpMDHh51 : 367 LpMDHh52: GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 289 LpMDHh53: GAATGTTTCAATCTACAAATCTCAAGMGNNTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 118 LpMDHh54 TAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA 40 LpMDHh55 ----ccntggaa-ccccnamgeca 20 LpMDHh56: TGCAGCCCCG-ATTGCA 16 LpMDHh57 LoMDHh58 : LpMDHh59 : LpMDHh61 : -----LpMDHh60 : LpMDHh62 : -----LpMDHh63 : -----LpMDHh64 : ----







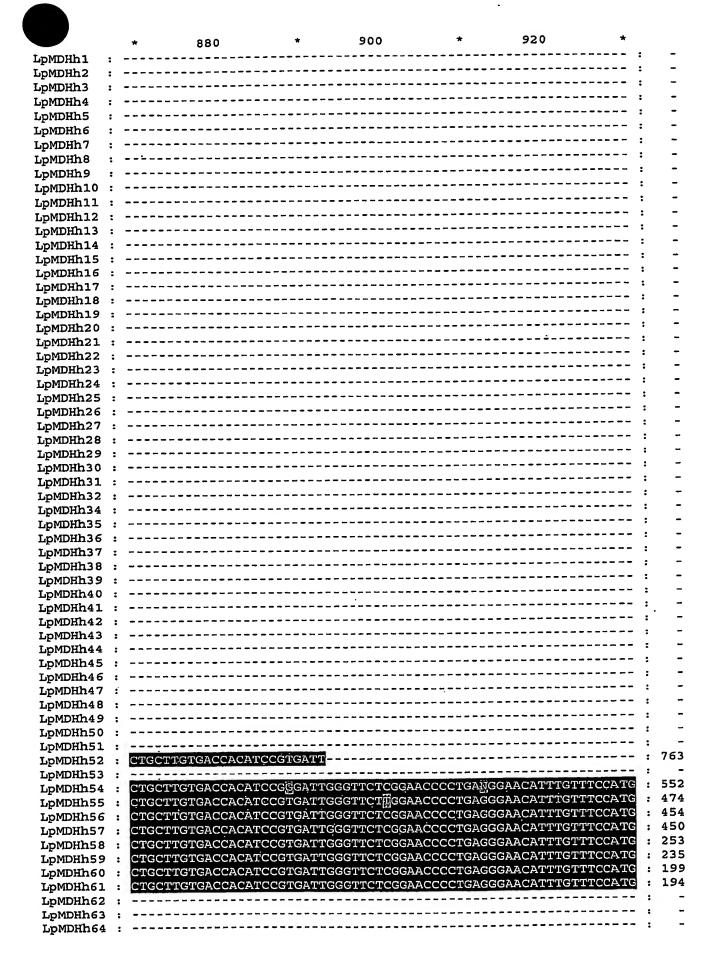
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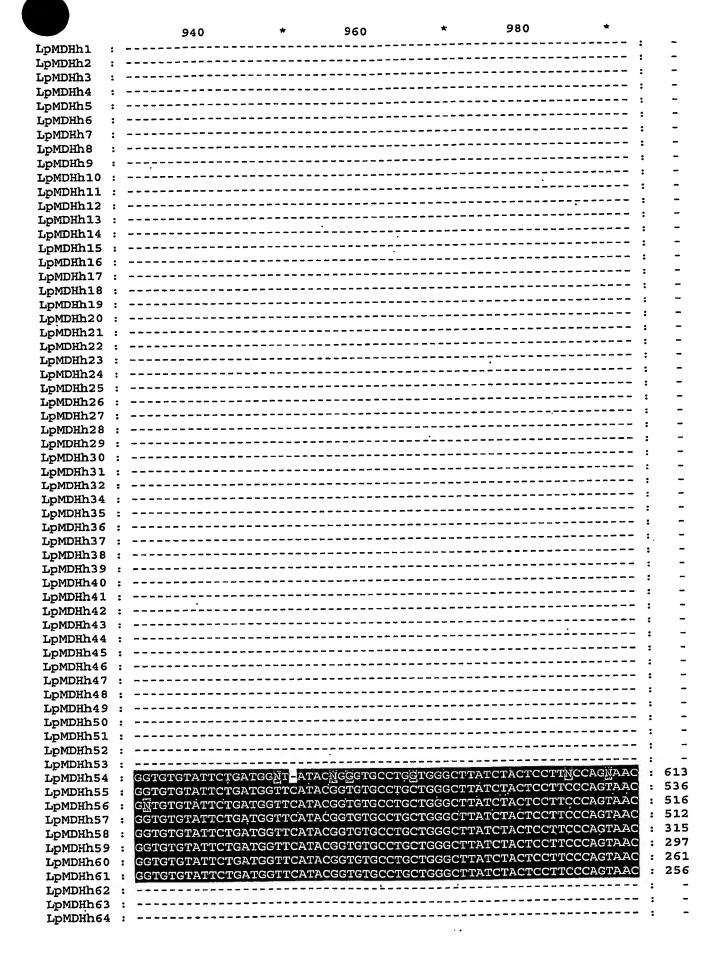
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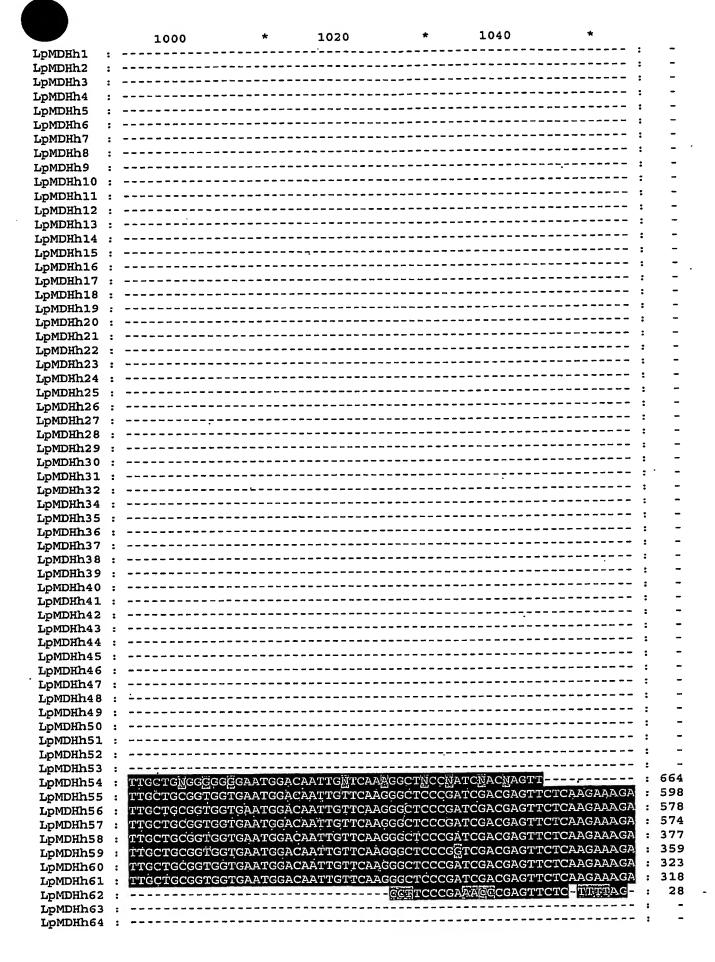
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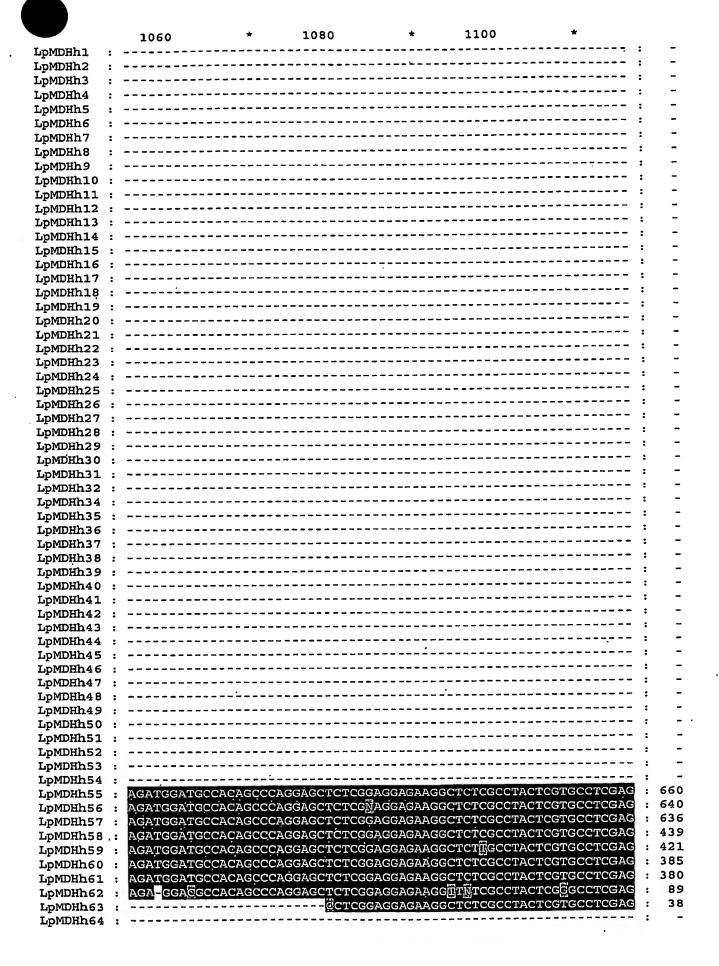
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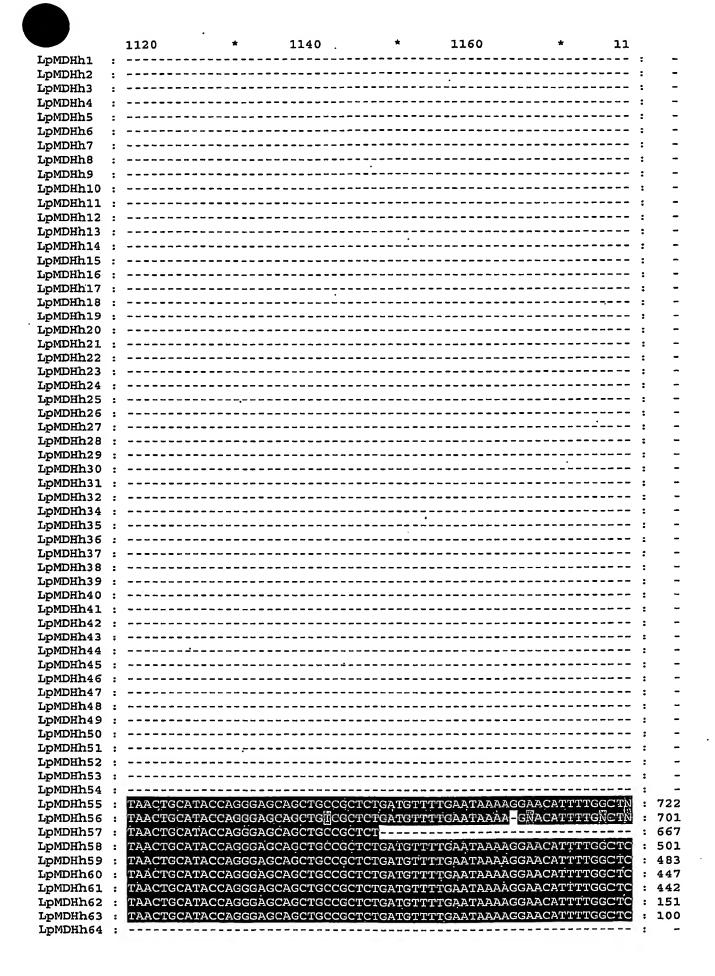
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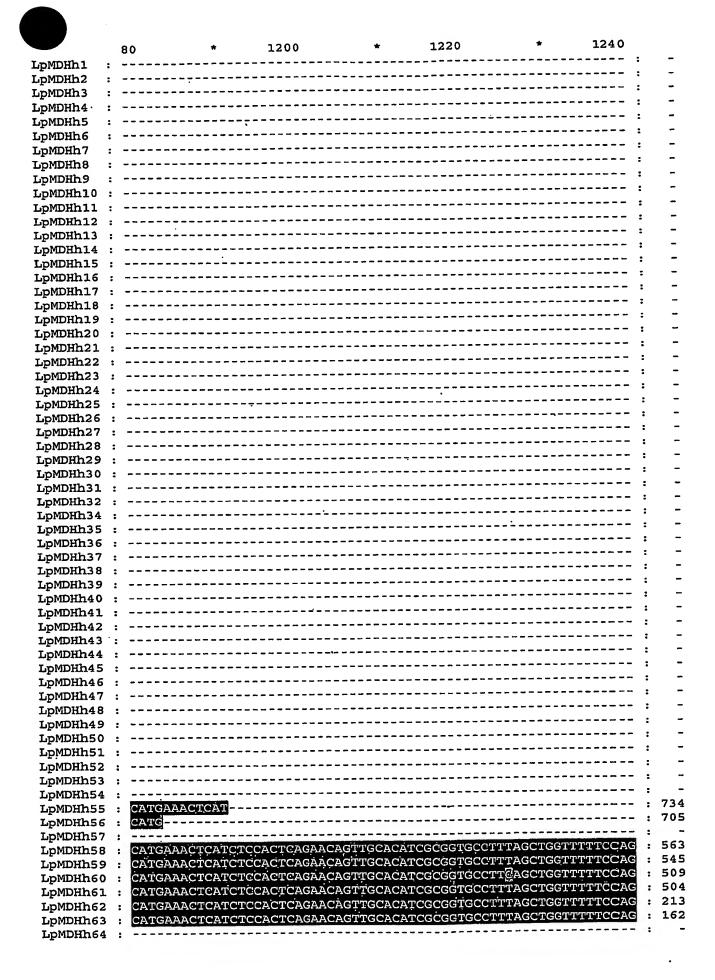


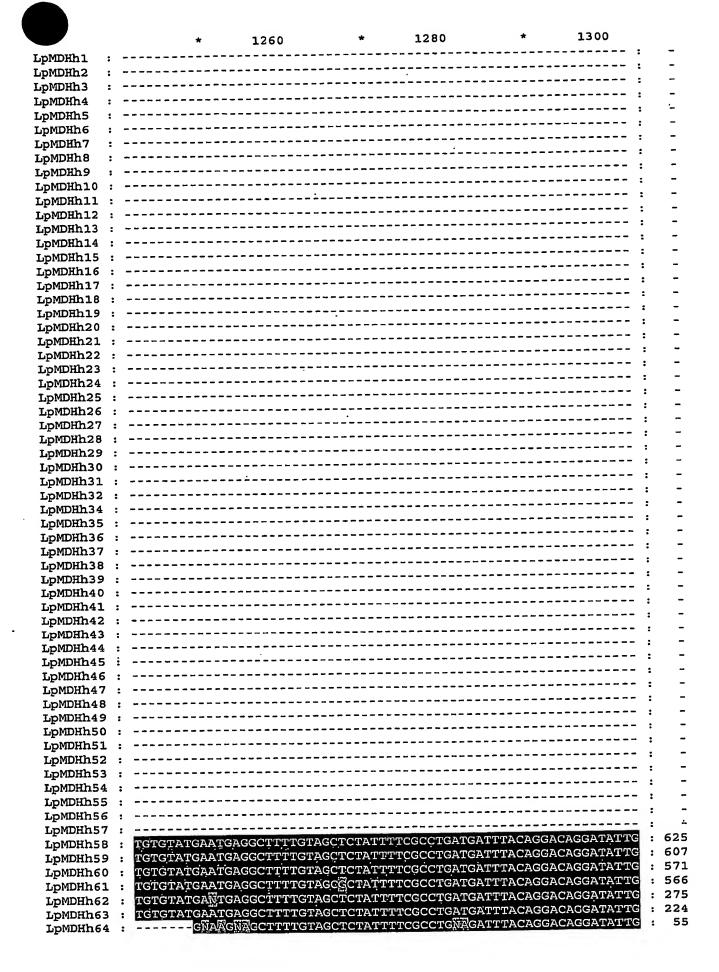












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LpMDHh37	:	;	-
LpMDHh38	:		
LpMDHh39	:		_
LpMDHh40	:		-
LpMDHh41	:		_
LpMDHh42	:		_
LpMDHh43	:	:	_
LpMDHh44	:		
LpMDHh45	:		_
LpMDHh46	:		_
LpMDHh47	:		-
LpMDHh48	:		_
LpMDHh49	:		_
LpMDHh50	:		_
LpMDHh51	:		_
LpMDHh52			_
LpMDHh53		::	_
LpMDHh54		:	_
LpMDHh55			_
LpMDHh56			_
LpMDHh57		A A A CCA A COTTOTA TO THE A A A A CCA A COTTOTA TO TATTO COCOTTOTA	687
LpMDHh58		GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACC	646
LpMDHh59		GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCA	633
LpMDHh60		: GCAGGAAGATIGGAACAATITGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACC	616
LpMDHh61		GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACC	337
LpMDHh62		GCAGGAAGATIGGAACAATITGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA	265
LpMDHh63		GCAGGAAGATTGGACAATTTGACGTCTGACAAAAAAAAAA	: 116
LpMDHh64	:	: GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACC	

1380 1400 LpMDHh1 LpMDHh2 LpMDHh3 LpMDHh4 LpMDHh5 LpMDHh6 LpMDHh7 LpMDHh8 LpMDHh9 LpMDHh10 LpMDHh11 LpMDHh12 LpMDHh13 LpMDHh14 LpMDHh15 LpMDHh16 LpMDHh17 LpMDHh18 LpMDHh19 LpMDHh20: LpMDHh21 LpMDHh22 LpMDHh23 LpMDHh24 LpMDHh25 LpMDHh26 LpMDHh27 LpMDHh28 LpMDHh29 LpMDHh30 LpMDHh31 LpMDHh32 LpMDHh34 LpMDHh35 LpMDHh36 LpMDHh37 LpMDHh38 LpMDHh39 LpMDHh40 LpMDHh41 LpMDHh42 LpMDHh43 LpMDHh44 LpMDHh45 LpMDHh46 LpMDHh47 LpMDHh48 LpMDHh49 LpMDHh50 LpMDHh51 LpMDHh52 LpMDHh53 LpMDHh54 LpMDHh55 LpMDHh56 LpMDHh57 LpMDHh58 LpMDHh59 LpMDHh60 LpMDHh61 LpMDHh62 LpMDHh63 TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCACGATATTGGCAGGA LpMDHh64

		* 1440 * 1460 * 1480		
LpMDHh1			:	-
LpMDHh2			:	-
LpMDHh3	•	**************************************	:	-
LpMDHh4	•		:	-
LpMDHh5	•		:	-
LpMDHh6	•		:	-
LpMDHh7	•		:	-
LpMDHh8	•		:	-
TDMDHU8	:		:	_
LpMDHh9	:		•	_
LpMDHh10	:		•	_
	:		:	_
LpMDHh12	:		:	_
<b></b>	:		:	_
LpMDHh14	:		:	_
	:		•	
-F	:			_
	:		:	_
LpMDHh18	:		:	-
	:		:	-
LpMDHh20	:		:	-
LpMDHh21	:		:	-
LpMDHh22	:	**************************************	:	-
LpMDHh23	:		:	-
LpMDHh24	:		:	-
LpMDHh25	:		:	-
LpMDHh26	•		:	-
LpMDHh27	:		:	-
LpMDHh28	:		:	-
LpMDHh29	:		:	-
LpMDHh30	:		:	-
LpMDHh31	:		:	-
LpMDHh32	:		:	_
	:		:	_
LpMDHh34	•		:	-
LpMDHh35	:		:	_
LpMDHh36	:		:	_
LpMDHh37	•	,	:	_
LpMDHh38	•		:	_
LpMDHh39	:		:	_
LpMDHh40	:		:	_
LpMDHh41	:		•	_
LpMDHh42	:		•	_
LpMDHh43	:		•	_
LpMDHh44	:		•	_
LpMDHh45	:		•	_
	:		:	_
LpMDHh47	:		:	_
LpMDHh48	:		•	_
LpMDHh49	:		•	_
LpMDHh50	:		•	_
LpMDHh51	:		:	_
LpMDHh52	:		:	_
LpMDHh53	:		:	-
LpMDHh54	:	***************************************	:	-
LpMDHh55	:		:	-
LpMDHh56	:		:	-
LpMDHh57	:		:	-
LpMDHh58	:		:	-
LpMDHh59	:		:	-
LpMDHh60	:	GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAA	:	750
LpMDHh61	:	0.0111001101111111111111111111111111111	:	-
LpMDHh62	:	GGATTGGAACAANNANANN	:	418
LpMDHh63	:		:	-
LpMDHh64	•	GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTAIITCTAAAAAAAAAA	:	236
Thuman 4	•			

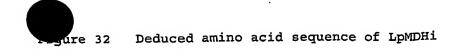
\* 20 \* 40 \* 60

LpMDHi : GTNCATAAAGCTGCCCAAAGCAATNCGTGNAATATTATCAGTAACCCTGTCAATTCTACC : 60

\* 80 \* 100 \* 120

LpMDHi : GTACCAATTGCTGCTGAAGTATTTAAAAAAAGCTGGGACATACAATNCTAAGAGATTGTTG : 120

\* 140 \* 160 \* LpMDHi : GGGGTTGACAACNGTTNGATGNNANTGACAGACCNTGCTCTTNGNNGNCGAGGTNCN : 177



LpMDHi : XHKAAQSNXXNIISNPVNSTVPIAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58

		*	20	*	40	*	60		
Lowoni		ANAAAGGAGCCGAC	GCAGGGGCGCA	GAATTCCAT	TGCTNACTC'	TGCCACCACCC	AAGTT	:	60
_p	•								
		*	80	*	100	* .	120		
LOMDHi		GGACATGGCGTCAG	CTGTTACAATC	AGTTCAGTC	AGCGCGCAGG	CCGCTTTGGTT	TCAAA	:	120
ראים ביים	•								
		*	140	*	160	*	180		
LAMDU		ACCAAGGAACCATG		TACAGTGGC		CATCGTCGTCG	ATCAG	:	180
לאתוקנה	•	ncommonate and	0000000						
			•						
•		*	200	*	220	*	240		
LOMDH		CTTCGAATCAGGAA				GGGCAACTGTT	ACCAC	:	240
прили	•	CIICOMICHOOM							
				•					
		*	260	*	280	*	300		
LOMDHA		AAGGGTTGTGCCAA		rgggtcgcag		AGGCATCTTAC	AAGGT	:	300
נגגלויינקם	•	AMOUGITOTOCOM							
		*	320	*	340	*	360		
LAMDES		GGCGGTGCTTGGTG	יריינריינפיינפני	TATCGGTCAA		TGCTGATCAAC	ATGTC	:	360
Cumudu	•	00000100110010			00.020000				
		*	380	*	400	*	420		
LOMDET		TCCTCTGGTCTCGG		татартатс		AGGGCGTCGCT	GCAGA	:	420
נווטויוקט	•	10010100101000							
		*	440	*	460	*	480		
LOMDHi		TCTCAGCCACTGCA		CAGGTCATG	GACTTCACTG	GCCCCGCAGA	CTAGC	:	480
رحبوت	•	10101.0001101001							
		*	500	*	520	*	540		
LoMDHi	:	AGAGTGCTTGAAAG	GTGTGGATGT	rgrcgrcatc	CCTGCGGGTG	TCCCAAGGAA	CCAGG	:	540
	•								
		*	560	*	580	*	600		
LpMDHi	:	CATGACCCGTGATC	ACCTTTTTAA	CATNAATGCG	GGAATCGNCA	AGTCGCTTAT	rgaggc	:	600
		*	620	*	640	*	660		
LpMDHj	:	TGTTGCAGACAATT	CCCTGAGGG	CCTTATTCAT	ATCATCAACA	ACCCCGGTCA	AACTCC	:	660
					•				

LpMDHj : CCCT : 664

LpMDHj : XRSRRRGAEFHLXTLPPPKLDMASAVTISSVSAQAALVSKPRNHGSTSYSGLKASSSSIS : 60

\* 80 \* 100 \* 120

LpMDHj : FESGTSFLGKTASLRATVTTRVVPKAKSGSQISPQASYKVAVLGAAGGIGQPLGLLIKMS : 120

LpMDHj : PLVSELRLYDIANVKGVAADLSHCNTPAQVMDFTGPAELAECLKGVDVVVIPAGVPRKPG : 180

LpMDHj : MTRDDLFNXNAGIXKSLIEAVADNCPEGLIHIINNPGQTPP : 221

1	ء.
	,

LpMDHk	:	* 20 * 40 * 60 TNTTTANCCCNCCAANTATCCAGNANCCACCTGGCCCTACACANAANAAAAACAAAAANN	:	60
LpMDHk	:	* 80 * 100 * 120 AACCAGNACGCAAGGGGGGGGGGGGGGGGGGGGGGGGATTCCCATCTGCTCACCAACCC	:	120
LpMDHk	:	* 140 * 160 * 180 AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGCT	:	180
LpMDHk	:	* 200 * 220 * 240 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG	:	240
LpMDHk	:	* 260 * 280 * 300 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTCGGGCGACTATC	:	300
LpMDHk	:	* 320 * 340 * 360 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	360
LpMDHk	:	* 380 * 400 * 420.  AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCAACCACTGGGCCTGCTGATCAAG		420
LpMDHk	:	* 440 * 460 * 480 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT	:	480
LpMDHk	:	* 500 * 520 * 540 GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	:	540
LpMDHk	:	* 560 * 580 * 600 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG	:	600
LpMDHk	:	* 620 * 640 * 660 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT	:	660
LpMDHk	:	* 680 * 700 * 720 GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	:	720
LpMDHk	:	* 740 * 760 * 780 TCCACTGTGCCGATTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	:	780
LpMDHk	. :	* 800 * 820 * 840 CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	:	840
LpMDHk	: :	* 860 * 880 * 900 AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT		900
LpMDHk	: :	* 920 * 940 * 960 CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG		960

DHK : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC : 1020 LpMDHk : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA : 1080 LpMDHk : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT : 1140 LpMDHk : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 1200 LpMDHk : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 1260

LpMDHk : AAG : 1263

LpMDHk	:	* 20 * 40 * 60 XLXXQXSXXHLALHXXKTKXNQXARGEPGRTQQFPSAHQPKLEMASAVTISSVSAQAALV	:	60
LpMDHk	:	* · 80 * 100 * 120 SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY	:	120
LpMDHk	:	* 140 * 160 * 180 KVAVLGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKGVAADLSHCNTPSQVMDFTGPAE	:	180
LpMDHk	:	* 200 * 220 * 240 LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN	•	240
LpMDHk	:	* 260 * 280 * 300 STVPIAAEILKQKGVYNPKKLFGVSTLDVVRANTFVAQKKNLSLIDVDVPVVGGHAGITI	:	300
LpMDHk	:	* 320 * 340 * 360 LPLLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA	:	360
LpMDHk	:	* 380 * 400 * 420 MAGDPDVYECTYVQSELTELPFFASRVKLGKDXVESIISSDLEGVTEYEAKALXALKAEL .	:	420

LpMDHk : K : 421

are 37 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHk

		* 20 * 40 * 60		
LpMDHk1	:	TNTTTANCCCNCCAANTATCCAGNANCCACCTG@CCCGAAGCA-AN-AAAAANAAAA&N	:	58
LpMDHk2	:	GNGCCGCACGGAANAAAANAAAANN GNCCCGCAAAGAAAAAAAAAA	:	28
LpMDHk3	:		:	27
LpMDHk4	:	GNCCEGCANGE AANAAANNAAAANN	:	27
LpMDHk5	:	GCCCCCANNCCAACAAAAAAAAANN	:	27
LpMDHk6	:		:	25
LpMDHk7	:		:	24
LpMDHk8	:	GÜTÜCAGAÜ-AAAAACCIVAAA@N	:	24
LpMDHk9	:		:	25
LpMDHk10	:		:	25
LpMDHk11	:	CCT-CANCG-A-ANAAAABE	:	22
LpMDHk12	:	TITIC CANADA CNAAAAN TEAN	:	24
LpMDHk13	:	TECCENAAAAANIIIIIAAG	:	23
LpMDHk14	:	ACACANAMNAAAAANN	:	22
LpMDHk15	:	ACACANAMNAAAAANN	:	22
LpMDHk16	:	ACACANÑÍ AA AAÑGAAAAAG	:	20
LpMDHk17	:	CAÑNNÃ AA AACAAAAAĞÜ	:	19
LpMDHk18	:	<b>ETT</b> CCAACAANGAAAAAG	:	21
LpMDHk19	:	GNACCACAAAA	:	20
LpMDHk20	:	SNACCAGAAAAAGA SNACCAGAAAAAGAGAAAAGG	:	20
LpMDHk21	:	GÑACGAGAAAA GAAAAAG GÑACGAGAAAA GAAAAAG	:	20 20
LpMDHk22 LpMDHk23	:	GNAGAAAAAGAAAANG CANANNAAAAAANN	:	19
LpMDHk24	•	CANANNAAAAANN		19
LpMDHk25		CANANINAAAAACAAAAANNCANANINAAAAACAAAAANN		19
LpMDHk26	:	CANANNAAAACAAAAANN		19
LpMDHk27	:	GACCAGAAAAA AAAAAAA	:	19
LpMDHk28	:	GICCAGAAAAAGAAAAAG		19
LpMDHk29	:	ANNA-AAAE NAAAAAEN		16
LpMDHk30	:	ANAWNAAAANCAAAAANN	:	18
LpMDHk31	:	NARARANAARANNA	:	17
LpMDHk32	:	NAAAAAAAANN	:	16
LpMDHk33	:	AÑNAAAÑCAAAANN	:	16
LpMDHk34	:	ладалалалада	:	16
LpMDHk35	:	GAAAAA A GAAAAA GAAAAA GAAAAAA GAAAAAA GAAAAAA	:	16
LpMDHk36	:	ANAAANCAAAANN	:	15
LpMDHk37	:	NAACANNIJAAA	:	11
LpMDHk38	:		:	11
LpMDHk39		AAAGCAAAANN	:	12
LpMDHk40		GNCAC ANAMN	:	10
LpMDHk41	:	GANGCANANN - GAGAGAAA	:	11
LpMDHk42	:		:	10
LpMDHk43	:	nnaaaaanan nraaaabjoraa	:	11 11
LpMDHk44 LpMDHk45	:	AAACAAAAAN		11
LoMDHk46	•	GACAANANN		-7
LpMDHk47	:	AANNAAAAAN		10
LpMDHk48	:	GN-NNAAN-		7
LpMDHk49		ANAMA -	:	6
LpMDHk50	:	ENACGAE	:	7
LpMDHk51	:	GANNIN-	:	6
LpMDHk52	:	Canann Eaccag	:	6
LpMDHk53	:		:	6
LpMDHk54	:		:	5
LpMDHk55	:		:	3
LpMDHk56	:		:	-
LpMDHk57	:		:	-
LpMDHk58	:		:	-
LpMDHk59	:		:	-
LpMDHk60	:		:	-
LpMDHk61	:		:	-
LpMDHk62	:		:	-
LpMDHk63	:		:	-
LpMDHk64	:		:	-
LpMDHk65 LpMDHk66	:		:	-
~Pi-iDUV0 0	٠		•	-

	*	80	*	100		120	
			GGGCGCACGCA				118
			GGGCGCACG <u>C</u> A				85
			GGGCGCACG <mark>-</mark> A				86
			GGGCGCACGCA				84
			GGGCGCACGCA				85
			GGGCGCACG <mark>-</mark> A				84
			GGGCGCACGCA				82
			GGGCGCACGCA				83
			GGGCGCACGCA				83
			GGGCGCACGCA				82
.1 : AGCEC .2 : NACC	CNIVEGGLAAGG	GGCGAGCCG	GGGCGCACG <mark>-</mark> A	GCAATTCCCA	TCTGCTCACC	AACCC:	81
2 : NACCA			GGGCGCACGCA				82
4 ACCA	NAG-GC-AGN	GGCGAGCCG	GGGCGCACGCA GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC:	81 80
5 : A-CCA		GGCGAGCCG	GGGCGCACGCA GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC:	79
6 : NACCA			GGGCGCACGCA GGGCGCACGCA				79
			GGGCGCACGCA				78
			GGGCGCACGCA				80
			GGGCGCACGCA				80
			GGGCGCACGCA				80
			GGGCGCACGCA				80
			GGGCGCACGCA				80
			GGGCGCACGCA				77
4 : ACCCZ	GNN-GC-AGG	GGCGAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC :	77
			GGGCGCACGCA				77
			GGGCGCACGCA				79
			GGGCGCACGCA				78
			GGGCGCACGCA				79
			GGGCGCACGCA				74
			GGGCGCACGCA				78
			GGGCGCACGCA				76
2 : ANCCA	GNA-GCAAGG	GGCGAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC:	75
3 : A-CCZ	GNACGCAAGG	GGCGAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC :	75
4 : AGCCA 5 : AGCCA	CEACCAAGG	CCCCA CCCG	GGGCGCACGCA GGGCGCACG <mark>-</mark> A	GCAATTCCCA	TCTGCTCACC	AACCC:	75
6 : A-CC	GNACGCAAGG	GGCGAGCCE	GGGCGCACGEA GGGCGCACGCA	GCAATICCCA CCAATTCCCA	TOTGOTCACO	AACCC :	74 74
7 : A	DUA A LA	GGCGAGCCG	GGGCGCACGCA GGGCGCACGCA	GCAATICCCA GCAATTCCCA	TCTGCTCACC	AACCC :	67
8 : AAAAN	- GAAAAAAGG	GGCGAGCCG	GGCGCAC <u>A</u> CA	CCAATTCCCA	TCTGCCCACC	AACCC :	70
	GNAEGCAAGG	GGCGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC :	72
O : AAAA	- GA'AAAAANG	GGCGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCCCACC	AACCC :	69
1 : AAAAA	NAAAAAAGGG	G-CGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCCCACC	AACCC :	70
2 : 🖾🖔	-GAAAAAAGG	GGCGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCCCACC	AACCC :	66
3 : ACCCA	G-ÑNGCAAGG	GGCGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC:	70
4 : NACCA	GNACGCAGGG	GGCGAGCCG	GGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC:	71
5 : A-CCA	GNACGCAAGG	GGCGAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC :	70
6 : AAAAA	TNAMAAAGG	GGCGAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCCCACC	AACCC:	68
7 : NACCA 8 : AAAAA	GNACGCAGGG	GGCCAGCCG	GGGCGCACGCA	GCAATTCCCA	TCTGCTCACC	AACCC :	70
9 AAAAA	T NAVAAANANG	GGCGAGCCG	GGCGCACGCA GGCGCACGCA	GCAATTCCCA	TCTGCCCACC	AVACCEC :	66
O : AAAAA	CANANAAA	GGCGAGCCG(	CCCCCCACCCA	CAATTCCCA	TCTGCCCACC	AACCC:	65
1 AAAAN	ENANAMAGG	GGCGAGCCG(	GGGCGCACGCA GGGCGCACGCA GGGCGCACGCA GGGCGCACGCA	CAATTCCCA	TCTGCCCACC	AACCC :	67
2 AAAAA	TATA A A A S CC	NACGAGCCGC	GGCGCACGCA	CAATICCCA	TCTGCGCACC.	AACCC :	66 65
3 AAAAA	GNDN A A A A CC	GCCAGCCGC	GGCGCACGCA GGCCCCACGCA	CANTICCCA	TOTGCGCACC	AACCC :	66
4 AAAAA	Nalala a Malico	GECGAGCCGC	GGCGCACGCA GGCGCACGCA GGGCGCACGCA	CAALICCCA	TCTGCGCACC.	AACCC :	64
5 : AAAAA	GNAANAAGG	GCGAGCCG	GGCGCACGCA GGCGCACGCA	CAATTCCCA	TCTGCCCACC	AACCC :	63
6 🗛	AAAANAANG	GGCGAGCCG	EGGCGCACGCA EGGCGCACGCA	CAATTCCCA	TCTGCCCACC	AACCC	57
7 : 💹	NNAAAAAAG	GGCGAGCCG	GGCGCACGCA	3CAATTCCCA	TCTGCCCACC	AACCC .	57
8 :	CAAGG	GGCGAGCCG	GGCGCACGCA(	CAATTCCCA	тстве <u>н</u> слес.	AACCC .	50
o . 9 :	ANAGG	GGCÑÑGCCG	eggggg-cgg-	G-AATT-CCA	TCTG-CCNCC	-A-CC:	43
0 :	MoM-1-1-	GGAGCCG	GGCMC-CGCA	CAATTCCCA	TCTGCTCACC	AACCC	42
٠		Held	*********	- ヘカ カ 中の へ へつ カリ	mamaaman	77000	37
2 :			NCA-GCA GNCXCN	CAATTCCCT	NCTGC@CACC	AACCC :	31
3 :			ENCACH	ACAJI TËCCON	NCTGCCCACC	AACCC :	31
				1			
4 : 5 :					TCTGC@CACC	AVACCC:	15

140 160 180 DHk1 178 LpMDHk2 145 LpMDHk3 aagttggacatcagctgttaccatcaglitcggtcagcgcgcagliccgctctgtggt 146 LpMDHk4 144 LpMDHk5 145 LpMDHk6 144 LpMDHk7 142 LpMDHk8 143 LpMDHk9 143 LpMDHk10 142 LpMDHk11 : 141 LpMDHk12 142 LpMDHk13 : 141 LpMDHk14 : 140 LpMDHk15 139 LpMDHk16  ${ t AAGTTGGAG}$   ${ t ATGGCATCAGCTGTTACC}$   ${ t ATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC}$ 139 aagttgg@natggcatcagctgttaccatcagctcagtcagcgcgcaggccgctttggtc LoMDHk17 138 AAGTTGGÄGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCCGTTGGTC LpMDHk18 : 140 LpMDHk19 140 LpMDHk20 : : 140 LpMDHk21 : 140 LpMDHk22 140 LpMDHk23 137 LpMDHk24 137 LpMDHk25 137 LpMDHk26 139 LpMDHk27 : 138 LpMDHk28 139 LpMDHk29 AAGTTGG<u>G</u>GATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC 134 LpMDHk30 138 LpMDHk31 : 136 LpMDHk32 : 135 LpMDHk33 : 135 LpMDHk34 135 LpMDHk35 134 LpMDHk36 134 LpMDHk37 : 127 LpMDHk38 130 LpMDHk39 AAGTTGGAĞATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCĞCAGGCCGCTTTGGT 132 AAGTTGGAĞATGGCATCAGCTGTĞACCATCAGTTCAGTCAGCGCĞCAGGCCGCTĞTGGTĞ AAGTTGGAĞATGGCATCAGCTGTĞACCATCAGTTCAGTCAGCGCCCAGGCCGCTĞTGGTÜ AAGTTGGAĞATGGCATCAGCTGÑĞACCATCAGTTCAGTCAGCGCĞCAGGCCGCTĞTGGTĞ LpMDHk40 129 LpMDHk41 130 LpMDHk42 : 126 LpMDHk43 130 LpMDHk44 131 LpMDHk45 130 LpMDHk46 128 LpMDHk47 130 LpMDHk48 126 LpMDHk49 125 LpMDHk50 : 127 ٤. LpMDHkS1 126 LpMDHk52 : 125 LpMDHk53 : 126 LpMDHk54 124 LpMDHk55 123 LpMDHk56 : 117 LpMDHk57 : 117 LpMDHk58 110 LpMDHk59 100 LpMDHk60 102 A TTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC
A NTTGGAÖATGGCATCAGCTGTÖACCATCAGÑTCAGTCAGCGCÖCAGGCCGCTÖTGGTÖ
ANTTGGA ATGGCATCAGCTGTÖACCATCAGÑTCAGTCAGCGCCCAGGCCGCTÖTGGTG
AAGTTGGAÖATGGCATCAGCTGTÖACCATCAGÑTCAGTCAGCGCCCAGGCCGCTÖTGGTÖ LpMDHk61 : 95 LpMDHk62 90 LpMDHk63 89 LpMDHk64 75 LpMDHk65 LpMDHk66

200 220 240 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG DHk1 238 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCGAAACCAAGGAATCATGGCAGCACGAGCTÜCGGTGGCCTAAAGGCATCATCGGCGTCG TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk2 LpMDHk3 206 LpMDHk4 204 TCGAPACCAAGGATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCGAPACCAAGGAATCATGGCAGCACGAGCTIICGGTGGCCTAAAGGCATCATCGGCGTCG TCGAPACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk5 205 LpMDHk6 204 LpMDHk7 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk8 : 203 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk9 : 203 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk10 : 202 TCGAAACCAAGGAATCATGGCAGCACÄAGCTÄCÄGTGGCCTAAAGGCATCATCÄÄCGTCG TCGAAACCAAGGAATCATGGCAGCACÄAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk11 201 LpMDHk12 202 LpMDHk13 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 201 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk14 200 LpMDHk15 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 199 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk16 199 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk17 198 LpMDHk18 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 200 LpMDHk19 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 200 LpMDHk20 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 200 LpMDHk21 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 200 LpMDHk22 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 200 LpMDHk23 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCAGCATCATCGTCG 197 LpMDHk24 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 197 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk25 197 LpMDHk26 TCGAAACCAAGGAATC<u>Ü</u>TGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 199 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk27 : 198 LpMDHk28: TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 199 LpMDHk29 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 194 LpMDHk30 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 198 LpMDHk31 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 196 LpMDHk32 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195 LpMDHk33 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195 LpMDHk34: TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCMAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCAAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTGAAGGCATCATCATCGTCG TCAAAACCAAGGAGTCATGGCAGCACGAGCTIICAGTGGCCTGAAGGCATCATCATCGTCG : 195 LpMDHk35 194 LpMDHk36: 194 LpMDHk37 : : 187 LpMDHk38 : : 190 LpMDHk39 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 192 TCMAAACCAAGGAGTCATGGCAGCACGAGCTIICAGTGGCCTGAAGGCATCATCATCGTCG TCMAAACCAAGGAGTCATGGCAGCACGAGCTIICAGTGGCCTGAAGGCATCATCATCGTCG TCMAAACCAAGGAGTCATGGCAGCACGAGCTIICAGTGGCCTGAAGGCATCATCATCGTCG LpMDHk40 : 189 LpMDHk41 : 190 LpMDHk42 : 186 TCGAAACCAAGGAÄTCATGGCAGCACÄAGCTÄCAGTGGCCTÄAAGGCATCATCATCGTCG LpMDHk43 190 LpMDHk44 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG 191 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCAAAACCAAGGAGTCATGGCAGCACGAGCTACAGTGGCCTGAAGGCATCATCATCGTCG TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG LpMDHk45 190 LpMDHk46 188 LpMDHk47 TCAAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAAGGCATCATCATCGTCG
TCAAAACCAAGGAGTCATGGCAGCACGAGCTICAGTGGCCTGAAGGCATCATCATCGTCG
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TCAAAACCAAGGAGTCATGGCAGCACGAGCTICAGTGGCCTGAAGGCATCATCATCGTCG 190 LpMDHk48 186 LpMDHk49: 185 LpMDHk50 187 LpMDHk51 186 LpMDHk52 TCANACCAAGGAGTCATGGCAGCACGAGCTLCAGTGGCCTGAAGGCATCATCATCGTCG
TCANAACCAAGGAGTCATGGCAGCACGAGCTLCAGTGGCCTGAAGGCATCATCATCGTCG
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TCANAACCAAGGAGTCATGGCAGCACGAGCTLCAGTGGCCTGAAGGCATCATCATCGTCG : 185 LpMDHk53 AAGGCATCATCATCGTCG 186 LpMDHk54 AAGGCATCATCATCGTCG : 184 LpMDHk55 : 183 LpMDHk56 : 177 LpMDHk57 : 177 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG T<mark>A</mark>AAACCAAGGAGTCATGGCAGCACGAGCTGCAGTGGCCTGAAGGCATCATCATCGTCG LpMDHk58 : 170 LpMDHk59 : 159 LpMDHk60 TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCGTCG
TCGAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG
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TCAAAACCAAGGAGTCATGGCAGCACGAGCTTTCAGTGGCCTGAAGGCATCATCATCGTCG
TCAAAACCAAGGAGTCATGGCAGCACGAGCTTTCAGTGGCCTGAAGGCATCATCATCGTCG : 162 LpMDHk61 : : 155 LpMDHk62 150 LpMDHk63 149 LpMDHk64 135 LpMDHk65 LpMDHk66

260 280 300 DHk1 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCACCTCTCTTCGGGCGACTATC : 298 LpMDHk2 265 atcagctt[jgaatcagggacatcgttcctgggcaagacjjgcctcecteegeggggctett LpMDHk3 266 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk4 264 LpMDHk5 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC ATCAGETTEGAATCAGGGACATCËTTCCTGGGCAAGACËGCCTCËCTËCGGGGGACTËTË : 265 LpMDHk6 264 LpMDHk7 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 262 LpMDHk8 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 263 LpMDHk9 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 263 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC ATCAGCTT[[GAATCAGGGACATCE]TTCCTGGGCAAGAC[[G]NCTCE]CTECGGGCGACTE]T[] ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk10 : : 262 LpMDHkl1: : 261 LpMDHk12: : 262 ATCAGCTTCGAATCAÑGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk13 261 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk14 260 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk15 : 259 LpMDHk16: ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 259 LpMDHk17 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 258 LpMDHk18 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 260 LpMDHk19 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 260 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk20 : 260 LpMDHk21 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260 LpMDHk22 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk23: : 257 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk24: 257 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk25 : : 257 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk26: : 259 LpMDHk27 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC ; 258 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk28 : : 259 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk29 : 254 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk30 : : 258 LpMDHk31 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 256 ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC LpMDHk32: : 255 LpMDHk33 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 255 LpMDHk34 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC 255 ATCAGCTTĬĬĠŖATCAGGGACATCĈŢTCCTGGGCAAGACĬĬĠCCTCĨĬĊŢĊGGGCGACŢĞŢĬĬ ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACŢĀTC LpMDHk35 : 254 LpMDHk36: ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC
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ATCAGCTTCGAATCIGGAACATCATTCCTGGGCAAGACIIGCCTCTTTCGGGCGICAGTC
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ATCAGCTTCGAATCÄĞGÄACATCATTCCTGGGCAAGACÄĞCCTCTCTTCGGGCGÄÇÄĞTC LpMDHk62 : : 210 LpMDHk63: : 209 LpMDHk64: 195 LpMDHk65 LpMDHk66 :

320 340 360 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC DHk1 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCIITAC ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk2 : 325 LpMDHk3 LpMDHk4 324 LpMDHk5 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 325 acc<u>@</u>caagattc<u>@</u>ceaaagcaaagtctggttctagac<u>a</u>acco LpMDHk6 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC ACCTCAAGGATTGTGCCAAAGGCAAAGGCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk7 322 ByHCMQT 323 LpMDHk9 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 323 LpMDHk10 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 322 acc<u>c</u>caaggattgtgccaaaggcaaagtctgggtctcagatatc<u>e</u>cctcaggc<u>a</u>tc<u>ii</u>tac LpMDHk11 : : 321 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATA1CACCTCAGGCCTCGTAC LpMDHk12 : 322 LpMDHk13: ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 321 LpMDHk14 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 320 LpMDHk15 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 319 LpMDHk16: ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319 LpMDHk17 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 318 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk18: 320 LpMDHk19 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 320 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk20 : 320 LpMDHk21 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC . 320 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk22 : 320 LpMDHk23 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 317 LpMDHk24 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 317 LpMDHk25 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 317 LpMDHk26:  ${ t ACCTC}$  AAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 319 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk27 : : 318 LpMDHk28: ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC • 319 LpMDHk29 :  ${\tt ACCTCAAGG}$  ATTGIGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 314 LpMDHk30 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 318 LpMDHk31 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 316 LpMDHk32 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 315 LpMDHk33 : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 315 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk34: 315 LpMDHk35 : ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCCCCTCAGGCATCCCTAC : 314 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk36 : 314 accccaaggattgtgccaaaggcaaagtctgggtctcagatatcccctcaggcAtclitac accccaaggattgtgccaaaggcaaagtctgggtctcagatatcccctcaggcAtclitac LpMDHk37: : 307 LpMDHk38 : 310 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk39: 312 ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCIITAC ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCIITAC ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCIITAC LpMDHk40 : : 309 LpMDHk41 : : 310 LpMDHk42 : : 306 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk43 : 310 LpMDHk44 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC
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ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCGTTAC
ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCGTTAC 311 LpMDHk45 : 310 LpMDHk46: : 308 LpMDHk47: 310 LpMDHk48 : 306 LpMDHk49 : 305 LpMDHk50 : : 307 LpMDHk51 : 306 LpMDHk52 : 305 LpMDHk53 : : 306 LpMDHk54 304 LpMDHk55 : 303 LpMDHk56 297 LpMDHk57 297 ACCTCAAGGATTGTGCCAAAGGCAAAGMCTGGGTCTCAGATATCACCTCAGGCCTCGTAC LpMDHk58 acc<u>ë</u>cëaggattgtgccaaaggcaaagtctgggtctcagatatc<u>ë</u>cctcaggc<u>ä</u>tcëtac LpMDHk59 279 LpMDHk60 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC 282 ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCĞCAGGCCTCGTAC ACCCCAGGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCĞCCTCAGGCATC∏TAC ACCCCAGGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCĞCCTCAGGCATC∏TAC ACCCCAGGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCĞCCTCAGGCATC∏TAC LpMDHk61 : 275 LpMDHk62 : 270 LpMDHk63 269 LpMDHk64: 255 LpMDHk65 LpMDHk66:

400 AAGGTGGCGGTGCTTGGTGCTG½CGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 418 DHk1 AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 385 LpMDHk2 AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGGCAACCACTGGGCCTGATCAAG LpMDHk3 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 384 LpMDHk4 AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG AAGGIJGGCGGTGCTTGGTGCTGCIJGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAJJ : 385 LpMDHk5 384 LpMDHk6 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 382 LpMDHk7 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383 LpMDHk8 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383 LpMDHk9 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG LpMDHk10 : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 381 LpMDHk11 : : 382 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG LpMDHk12 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 381 LpMDHk13 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk14 : : 379 LpMDHk15 : AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379 LpMDHkl6: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 378 LpMDHk17 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk18 : AAGGTGGCGGTGCTTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk19 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk20: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk21 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 380 LpMDHk22 : AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 377 LpMDHk23 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 377 LpMDHk24 : AAGGTGGCGGTG[jjTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG LpMDHk25 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG . 379 LpMDHk26 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGA<u>C</u>CAAG LpMDHk27: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 379 LpMDHk28: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 374 LpMDHk29: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 378 LpMDHk30 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 376 LpMDHk31 : AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG LpMDHk32 : 375 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG LpMDHk33 : AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 375 LpMDHk34: AAGGTGGCGGTGCTTGGTGCTGCÄGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 374 LpMDHk35 : : 374 LpMDHk36 AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 367 LpMDHk37: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 370 LpMDHk38: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 372 LpMDHk39: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 369 LpMDHk40 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 370 LpMDHk41: AAGGTGGÏGGTGCTTGGTGCTGCÏGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 366 LpMDHk42: : 370 LpMDHk43: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 371 LpMDHk44: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370 LpMDHk45 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 368 LpMDHk46: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370 LpMDHk47: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366 LpMDHk48: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGT[]AACCACTGGGCCTGCTGATCAAG : 365 LpMDHk49 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 367 LpMDHk50 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 366 LpMDHk51 : : 365 LpMDHk52: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366 LpMDHk53 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 364 LpMDHk54 AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 363 LpMDHk55 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 357 LpMDHk56: AAGGTGGCGGTGCTTGGTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 357 LpMDHk57: AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 350 LpMDHk58 AAGGTGGCGGTGCTTGGTGCTGC[[GGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 339 LpMDHk59 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 342 LpMDHk60 AAGGTGGCGGTGCTTGGTGCTGCCGGTGATCACHTGCHCTGGGCCTGCTGATCAAG AAGGTGGCGGÄGCTTGGTGCTGÄGGÄGGCATÄGGÄCAACCACTGGGCCTGCTGATÄAAG AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 335 LpMDHk61 : : 330 LpMDHk62 329 LpMDHk63 AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 315 : LpMDHk64 TTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG 47 LpMDHk65

LpMDHk66

440 460 480 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGACAATGTCAAGGGAGTCGCT DHk1 478 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk2 445 LpMDHk3 atgtctcctctägtctcagagctgcgcctgtatgatattgccaatgtcaagggggtcgct 446 LpMDHk4 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 444 LpMDHk5 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 445 LpMDHk6 ATGTCTCCTCTGGTCTCAN-----LpMDHk7 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 442 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk8 443 LpMDHk9 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 443 LpMDHk10 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 442 atgtctcctctggtctcagagctgcgcctgtatgatattgccaatgtcaaggg@gtcgct LpMDHk11 441 LpMDHk12 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk13 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 441 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk14 440 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk15 439 LpMDHk16 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 439 LpMDHk17 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 438 LpMDHk18 :  ${ t ATGTCTCCTCTGGTCTCAG} { t AGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT}$ 440 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk19 440 LpMDHk20: ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 440 LpMDHk21 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 440 LpMDHk22 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 440 LpMDHk23 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 437 LpMDHk24 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 437 LpMDHk25 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 437 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk26 : 439 LpMDHk27: ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 438 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk28 : 439 LpMDHk29 atgtctcctctggtctcaga<u>a</u>ctgcgcctgtatgatattgccaatgtcaagggagtcgct 434 LpMDHk30 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 438 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk31 : 436 LpMDHk32 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 435 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk33 : 435 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk34: 435 atgtctcctctggtctca<u>n</u>agctgcgcctgtatgatattgccaatgtcaaggg<u>ë</u>gtcgct LpMDHk35 : 434 atgtctcctctggtctcagagctgcgcctgtatgatattgc<u>c</u>aatgtcaagggagtcgct LpMDHk36 : 434 LpMDHk37 atgtcectctggtctcegagctgcgcctgtatgatattgceaatgtcaagggeggtcgct atgtcectctggectcegagctgcgcctgtatgatattgceaatgtcaagggegtcgct : 427 LpMDHk38 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT 430 LpMDHk39 : 432 LpMDHk40 429 LpMDHk41 : 430 LpMDHk42 426 LpMDHk43 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT 430 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk44 431 ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT LpMDHk45 430 LpMDHk46 atgtcgcctctggtctcggagctgcgcctgtatgatattgcgaatgtcaagggggtcgct 428 LpMDHk47 atgtctctctggtctcagagctgcgcctgtatgatattgccaatgtcaagggagtcgct ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT
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		* 500		520	*	540	
DHk1:		AGNCACTGCAACA					: 538
LpMDHk2:		AGCCACTGCAACA					: 505
LpMDHk3:		AGCCACTGCAACA					: 506
LpMDHk4 :		AGCCACTGCAACA					: 504
LpMDHk5 :	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT	CACTGGCCCAC	GCAGAA	: 505
LpMDHk6 :							:
LpMDHk7:		AGCCACTGGAACA					: 502
LpMDHk8 :		AGCCACTGCAACA				_	: 503 : 503
LpMDHk10 :		AGCCACTGCAACA AGCCACTGCAACA					: 503
LpMDHk11 :		AGCCACTGCAACA AGCCACTGCAACA					: 501
LpMDHk12:		AGCCACTGCAACA					: 502
LpMDHk13 :		AGCCACTGCAACA					: 501
LpMDHk14 :		AGCCACTGCAACA					: 500
LpMDHk15 :	2	AGCCACTGCAACA					: 499
LpMDHk16 :		AGCCACTGCAACA					: 499
LpMDHk17:		AGCCACTGCAACA					: 498
LpMDHk18 :	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT(	CACTGGCCCA	GCAGAA	: 500
LpMDHk19 :	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT	CACTGGCCCAC	GC <mark>I</mark> GAA	: 500
LpMDHk20 :		AGCCACTGCAACA					: 500
LpMDHk21 :		AGCCACTGCAACA					: 500
LpMDHk22 :		AGCCACTGCAACA					: 500
LpMDHk23 : LpMDHk24 :		AGCCACTGCAACA					: 497
LpMDHk25 :		agccgctgcaaca agccactgcaaca					: 497 : 497
LpMDHk26 :		AGCCACTGCAACA					: 499
LpMDHk27 :		AGCCACTGCAACA					: 498
LpMDHk28 :		AGCCACTGCAACA					: 499
LpMDHk29 :		AGCCACTGCAACA					: 494
LpMDHk30 :	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT	CĂCTGGCCCA	GCAGAA	: 498
LpMDHk31 :	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT	CACTGGCCCA	GCAGAA	: 496
LpMDHk32:		AGCCACTGCAACA					: 495
LpMDHk33 :		AGCCACTGCAACA					: 495
LpMDHk34 :		AGCCACTGCAACA					: 495
LpMDHk35 :		AGCCACTGCAACA					: 494
LpMDHk36 : LpMDHk37 :		AGCCACTGCAACA AGCCACËGCAACA					: 494 : 487
LpMDHk38:	GCGGATCTC	AGCCACTGCAACA	CCCCTGCTCAC	GICAIGGACII GTCATGGACTT	CACIGGCCCC	CCCAA	: 487
LpMDHk39:		AGCCACTGCAACA					: 492
LpMDHk40 :		AGCCACTGCAACA					: 489
LpMDHk41 :	4.4	AGCCACTGCAACA	2.0				: 490
LpMDHk42 :	GCAGATCT[]	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT	CACTGGCCCCC	GCGGAA	: 486
LpMDHk43:	GCAGATCTC	AGCCACTGCAACA	CGCCTTCTCAG	GTCATGGACTT(	CACTGGCCCAC	GCAGAA	: 490
LpMDHk44:		AGCCACTGCAACA					: 491
LpMDHk45 :		AGCCACTGCAACA					: 490
LpMDHk46 : LpMDHk47 :		AGCCACTGCAACA AGCCACTGCAACA					: 488
LpMDHk48:		AGCCACTGCAACA AGCCACTGCAACA					: 490
LpMDHk49:	GCGGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTT	CACTGGCCCC	CCGAA	: 485
LpMDHk50 :	GCCGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTT	CACTGGCCCC	CCGAA	: 487
LpMDHk51 :	GCGGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTT(	CACTGGCCCC	CGGAA	: 486
LpMDHk52 :	GCCGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTT	CACTGGCCCC	CGGAA	: 485
LpMDHk53 :	GCCGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	<b>ፕፕሮልጥናርል</b> ርምጥ	TACTEGECCC	CCCAA	: 486
LpMDHk54:	GCCGATCTC	AGCCACTGCAACA	CGCCTCCTCAG	GTCATGGACTT	CACTGGCCCC	CCGAA	: 484
LpMDHk55 :	GCCGATCTC	AGCCACTGCAACA	CGCCTGCTCAG	STCATGGACTTO	CACTGGCCC	GCGGAA	: 483
LpMDHk56:		AGCCACTGCAACA					: 477
LpMDHk57:	GCGGATCTCA	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTT(	CACTGGCCCg	CGGAA	: 477
LpMDHk58 : LpMDHk59 :		AÑICACTGCAACA AGCCACTGCAACA					: 470
LpMDHk59 :		AGCCACTGCAACA AGCCACTGCAACA					: 459
LpMDHk61:		AGCCACTGCAACA AGCCACTGCAACA					: 462 : 455
LpMDHk62 :							: 45:
LpMDHk63:	GCGGATCTCA	AGCCACTGCAACA	CGCCTGCTCAG	GTCATGGACTTC	CACTGGCCCCC		· 449
LpMDHk64:	GCCGATCTC	AGCCACTGCAACA	CGCCTÉCTCAG	GTCATGGACTT	CACTGGCCCGG	CGGAA	: 435
LpMDHk65 :	GCAGATCTCA	AGCCACTGCAACA	CGCCTGCTCAG	SCATGGACTTC	-ACTGGCCC	CGGAA	: 167
LpMDHk66:	EATC	AGCC: CTGCAACA	DADTOËTODDO.	GCATGGACTT	CACTGGCCCC	CGGAA	: 54

560 580 600 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGÄCATCCCTGCGGGTGTÄCCAAGGAAG MDHk1 LpMDHk2 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 565 LpMDHk3 CTAGC@GACTGCTTGAAAGGTGT@GATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 566 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTC<u>F</u> LpMDHk4 564 LpMDHk5  $\mathtt{CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG}$ 565 LpMDHk6 LpMDHk7 561 LpMDHk8 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 563 ctagctg@ctgcttgaaaggtgttgatgttgtcgtcatccctgcgggtgtcccaaggaag LpMDHk9 563 LpMDHk10 :  ${ t CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ 562 LpMDHk11 : ctagc@gactgcttgaaaggtgt@gatgttgtcgtcatccctgcgggtgtcccaaggaag : 561 LpMDHk12  ${ t CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ : 562 LpMDHk13 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTC<u>;;</u>CAAGGAAG : 561 LpMDHk14 : : 560 LpMDHk15 : 559 LpMDHk16 :  ${ t CTAGC}{ t TGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG}$ : 559 LpMDHk17:  $\tt CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ : 558 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk18: : 560 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk19 : 560 : LpMDHk20 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 560 LpMDHk21 :  $\tt CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ 560 LpMDHk22 : 560 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk23 : 557 LpMDHk24 : ctagctgactgcttga\begagtgttgatgttgtcgtcatccctgcgggtgtcccaaggaag 557 LpMDHk25 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 557 LpMDHk26 :  $\mathtt{CTAGC}$   $\mathtt{TGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ : 559 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk27 : : 558 СТАGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG СТАGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTҊССААGGAAG LpMDHk28 : : 559 LpMDHk29 : 554 LpMDHk30 :  $\mathtt{CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG}$ 558 LpMDHk31 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 556 LpMDHk32 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555 LpMDHk33 :  ${ t CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ : 555 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk34 : 555 LpMDHk35 : CTAGC@GACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 554 CTACCTGACTGCAAAGGTGTTGATGTTGTCGTCATCCTGCGGGTGTCCCAAGGAAG CTAGCAGAGTGCTTGAAAGGGGTGTGATGTTGTCGTCATCCCTGCGGGTGTMCCAAGGAAG CTAGCAGAGTGCTTGAAAGGGGTGGATGTTGTCGLATCCCTGCGGGTGTMCCAAGGAAG CTAGCTGACTGCTTGAAAGGCGTGATGTTGTCGTCATCCTGCGGGTGTCCCCAAGGAAG LpMDHk36 554 LpMDHk37: : 547 LpMDHk38 : : 549 LpMDHk39 : 551 CTAGCÄGAĞTGCTTGAAAGGĞGTĞGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG CTAGCÄGAĞTGCTTGAAAGGĞGTĞGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAĞ CTAGCĞGACTGCTTGAAAGGTGTĞGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk40 : : 549 LpMDHk41 : 550 LpMDHk42: : 546 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk43 : 550 LpMDHk44 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 551 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk45: : 550 ctagc\deltagatgtgcttgaaagg\deltagatgttgtcgtcatccctgcgggtgtcccaaggaag LpMDHk46: 548 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk47: CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTGTGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTGGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
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CTAGCÄGAGTGCTTGAAAGGGTTGATGTTGTCGTCATCCTTGCGGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGATTGTCGTCATCCTTGCGGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGGATGTTGTCGTCATCCCTGCGGTGTCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGGATGTTGTCGTCATCCCTGCGGTGTCCCCAAGGAAG
CTAGCÄGAGTGCTTGAAAGGGTTGGATGTTGTCGTCATCCCTGCGGTGTCCCCAAGGAAG 550 LpMDHk48 : 546 LpMDHk49 545 LpMDHk50 547 LpMDHk51 : 546 LpMDHk52: 545 LpMDHk53 : 546 LpMDHk54 544 LpMDHk55 : 543 LpMDHk56: 537 LpMDHk57: 537 CTA----LpMDHk5B 473 CTAGCEGACTGCTTGAAAMGTGTEGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk59 519 LpMDHk60 CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG 522 LpMDHk61 :  $\tt CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG$ 515 LpMDHk62 : CTAGCAGAGTGCTTGAAAGGGGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG CTAGCAGAGTGCTTGAAAGGGGTGGATGTTGNCGTCATCCCTGCGGGTGTCCCAAGGAAG CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG LpMDHk63: 509 LpMDHk64: 495 LpMDHk65 227 • LpMDHk66

620 660 Hk1 CATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNNAAGTCGCTTATT 658 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT CCEGGCATGACECGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATE LpMDHk2 625 LpMDHk3 : 626 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk4 624 LpMDHk5 CCAGGCA@GACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 625 LpMDHk6 LpMDHk7 LpMDHk8 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 623 LpMDHk9 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 623 LpMDHk10 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 622 CCEGGCATGACECTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk11 : 621 LpMDHk12 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 622 LpMDHk13 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 621 LpMDHk14 :  ${\tt CCAGGCATGACCCGTGATGACCTTT}{\tt TTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ : 620 LpMDHk15 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk16 : 619 LpMDHk17:  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 618 LpMDHk18 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 620 LoMDHk19 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNCAAGTCGCTTATT 620 LpMDHk20 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ : 620 LpMDHk21 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 620 LpMDHk22 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 620 LpMDHk23 : CCAGGCATGACCCATGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 617 LpMDHk24 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 617 LpMDHk25 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 617 LpMDHk26 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 619 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk27: 618 LpMDHk28 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 619 LpMDHk29 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 614 LpMDHk30 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 618 LpMDHk31 :  ${ t CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 616 LpMDHk32 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 615 LpMDHk33:  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 615 LpMDHk34 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 615 <u>CCÜGGCATGACÜCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATÇ</u> LpMDHk35 : 614 LpMDHk36: CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 614 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGG-CATCGTC-AGÑÑGCTTATC LpMDHk37 : 605 LpMDHk38 : CCAGGCATGACCCGTGATGACCTTTÄTAACATCAATGCGGGCATCGÄCÄAGÄCGCTTATC 609 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk39 : 611 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk40 : 609 LpMDHk41 : 610 CCÄGGCATGACÍÏCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGÑCAÑCTĞCCĞTGAĞGĞCÜTÇÄTÇGAÏATCAÏCAGCAACÇCGGTCAAĞTCÇAĞTĞTĞ CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk42: 606 LpMDHk43 : 610 LpMDHk44: 611 LpMDHk45 :  ${\tt CCAGGCATGACCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 610 LpMDHk46: CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC 608 LpMDHk47 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 610 LpMDHk48 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTAT 606 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk49 605 LpMDHk50 607 LpMDHk51 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTAT 606 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk52 605 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk53: 606 LpMDHk54: 604 LpMDHk55 : 603 CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCNATGCGGGCATCGTCAAGTCGCTTATC LpMDHk56 597 LpMDHk57 597 LpMDHk58 CCHGGCATGACHCGTGATGACCTTTTTAACATCAATGCGGGCATCGCCAAGTCGCTTATC LpMDHk59 579 LpMDHk60: CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 582 LpMDHk61 :  ${\tt CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT}$ 575 LpMDHk62: CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC LpMDHk63: 569 LpMDHk64: 555 LpMDHk65: CCIIGGCATGACIICGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT 287 CCIÏGGCATGACIÏCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT LpMDHk66

MODINA 4  AGRICATOR TO CARGA CARACTECCT GAGGCETT CATTCATTATATACACAACCCGGTCAAC   MODINA 6  MODINA 6  MODINA 7  MODINA 8  AGRICATOR CARGACACACTECCCT GAGGCCT TO ATCCATATCATTCAGCAACCCGGTCAAC   MODINA 8  MODINA 9  MODINA 11  AGRICATOR CARGACACACTECCCT GAGGCCT TO ATCCATATCATCAGGAACCCGGTCAAC   MODINA 9  MODINA 9  MODINA 11  AGRICATOR CARGACACACTECCCT GAGGCCT TO ATCCATATCATCAGGAACCCGGTCAAC   MODINA 13  AGRICATOR CARGACACACTGCCCT GAGGCCT TO ATCCATATCATCAGGAACCCGGTCAAC   MODINA 13  BAGGCT GAT TO GAGAACAACTGCCCT GAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 15  MODINA 15  MODINA 15  MAGGCT GAT TO GAGAACAACTGCCCT GAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 15  MODINA 17  MAGGCT GAT TO GAGAACAACTGCCCT GAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 17  MAGGCT GAT TO GAGAACAACTGCCCT GAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 17  MAGGCT GAT TO GAGAACAACTGCCCT GAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 17  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 19  MODINA 19  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 20  MODINA 21  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 23  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 24  MODINA 23  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 24  MODINA 25  MAGGCT GAT TO ATCCATACATCAGGCCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 25  MODINA 25  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 25  MODINA 26  MODINA 27  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 27  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 27  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 27  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGTCAAC   MODINA 27  MODINA 27  MODINA 27  MAGGCT GAT TO ATCCATACATCAGGACCT TO ATCCATATCAT CAGGAACCCGGT	_			
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MOBIRS 2  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATCAGCAACCGGTCAAC MOBIRS 3  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATCAGCAACCGGTCAAC MOBIRS 4  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATCAGCAACCGGTCAAC MOBIRS 5  MOBIRS 5  MOBIRS 6  MOBIRS 7  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATCAGCAACCGGTCAAC MOBIRS 8  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATCAGCAACCGGTCAAC MOBIRS 1  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATATCATACAGCAACCGGTCAAC MOBIRS 1  AGGCTGTTGCAGACAACTGCCCTTAAGGCTTCATTCATACATA	OUT 1			•
MODIRA: 3		•		:
MODIRA   GAGGCTGTGTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   MODIRA   GAGGCTGTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   MODIRA   GAGGCTGTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   MODIRA   GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MODIRA   GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATC	LpMDHk3			:
MODILES   GAGGETTETGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGGTCAAC   MODILES   GAGGETGTTGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGGTCAAC   MODILES   GAGGETGTTGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGGTCAAC   MODILES   GAGGETGTTGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGGTCAAC   MODILES   GAGGETGTTGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGTCAAC   MODILES   GAGGETGTTGEAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCGGTCAAC   MODILES   GAGGETGTTGEAGACAAACTGCCCTGAGGCCTTCATCCATATCATCAGGAACCCGGTCAAC   MODILES   GAGGETGTTGEAGACAAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGTCAAC   MODILES   GAGGETGTTGEAGACAAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGTCAAC   MODILES   GAGGETGTTGCAGACAAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCGGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGGTCAAC   MODILES   GAGGETGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGGTCAAC   MODILES   GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGAACCCGGGTCAAC   MODILES   GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGCAACCCGGGTCAAC   MODILES   GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGGCAACCCGGGTCAAC   MOD	LpMDHk4	:		:
MDBBHR 9	LpMDHk5	:	GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	:
MDBHAB : GAGGGTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA10 : GAGGGTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA11 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA16 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA17 : GAGGGTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC   MDBHA12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC   MDBHA13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC   MDBHA14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC   MDBHA13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC   MDBHA13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC   MDBHA14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC   MDBHA14 : GAGGCTGTTGCAGACAACTGCCCTG	LpMDHk6	:		:
MDBHES : GAGGCTGTTGCAGACAACTĞCCCTTAGGCCTTCATCCATATCATCAGCAACCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATATCATCAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATACAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATACAGCAACCCGGTCAAC MDBHES : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATACACACAC	LpMDHk7	:		:
MDMH:10 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:11 : GAGGCTGTTGCAGCACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:17 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:17 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATACAACACCGGTCAAC MDMH:19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATACAACCAGGTCAAC MDMH:19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:10 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCACACACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTTCGAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTTCCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC MDMH:13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC MDMH:14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCAGCAACCCGGTCAAC MDMH:14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGA	LpMDHk8	:		:
MOBBRIL1 : GAGGCTGTTGCAGACACTGCCCTTAGCCCTTATCATCATCATCAGCAACCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTTAGGCCTTCATCATTATCATCAGCAACCCCGGTCAAC MOBBRIL4 : GAGGCTGTTGCAGACAACTGCCCTTGAGGCCTTCATTGCATATCAGCAACCCCGGTCAAC MOBBRIL4 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATTGCATATCATCAGCAACCCCGTCAAC MOBBRIL5 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATTGCATATCATCAGCAACCCCGTCAAC MOBBRIL5 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATTCCATATCATCAGCAACCCCGTCAAC MOBBRIL5 : GAGGCTGTTGCAGACA MOBBRIL5 : GAGGCTGTTGCAGACA MOBBRIL5 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC MOBBRIL5 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC MOBBRIL2 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC MOBBRIL2 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAACACACCCCGGTCAAC MOBBRIL2 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCAGCAACCCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATATCATCAGCAACCCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATATCATACACAACCACCCGTCCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC MOBBRIL3 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC MOBBRIL	LpMDHk9	:		:
DADBIR12   GAGGETGTTECAGRACACTGCCCTGAGGCCTTCATTCATTCATCACAACCCGGTCAAC pMDIR13   GAGGETGTTECAGACAACTGCCCTGAGGCCTTCATTCATTCATCACCAACCCGGTCAAC pMDIR15   GAGGETGTTECAGACAACTGCCCTGAGGCCTTCATTCATTCATCACCAACCCGGTCAAC pMDIR15   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATTCATTCATCACCAACCCGGTCAAC pMDIR16   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR17   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR18   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR19   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTECAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATCACCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCACCAACCCGGTCAAC pMDIR12   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCATTATCATCACCAACCCCGGTCAAC pMDIR13   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCATTATCATTCACACAACCCCGGTCAAC pMDIR13   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCATTATCATTCACCACACCCCGGTCAAC pMDIR13   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCATTATCATCACCAACCCCGGTCAAC pMDIR13   GAGGTGTTTCAGACAACTGCCCTGAGGCCTTCATCATTATCATTCACCAACCA	LpMDHk10	:		:
DMDH:13 : DAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCATTCAT	-	:	-	:
DMDH:14 : DAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATGCATATCATCAGCAACCGGTCAGE DMDH:15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAGC DMDH:17 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DMDH:18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:23 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:23 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:26 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATTATCATCAGCAACCCGGTCAAC DMDH:34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DMDH:35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DMDH:36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATTATCAGCAACCCGGTCAAC DMDH:46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTC	•	:		:
DMDH:15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:17 : GAGGCTGTTGCAGACAACTGGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:18 : GAGGCTGTTGCAGACATGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:10 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:10 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTCATCAGCAACCCGGTCAAC DMDH:14 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DMDH:14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DMDH:14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DMDH:14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAAC	-	:	1.4	:
DNDHK16 : DAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DAMDHK17 : GAGGCTGTTGCAGACACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK21 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK22 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK22 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DAMDHK23 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DAMDHK24 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK25 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK26 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DAMDHK31 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DAMDHK32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DAMDHK33 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC DAMDHK33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK33 : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTCATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DAMDHK36 : GAGGCTGTTGCAGC	-	:	hef beam	:
DNDHK17 : GAGGCTGTTGCAGACA- DNDHK18 : GAGGCTGTTGCAGACA- DNDHK19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK19 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK12 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK12 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK12 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCAGCAACCCGGTCAAC DNDHK13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DNDHK13 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DNDHK13 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DNDHK14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC DNDHK14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC	-	:		:
DMDH:18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC DMDH:19 : GAGGCTGTGCGAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:21 : GAGGCTGTTGCGAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDH:22 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:23 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:23 : GAGGCTGTTGC DMDH:23 : GAGGCTGTTGC DMDH:25 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:25 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:25 : GAGGCTGTTGCAGCAACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:26 : GAGGCTGTTGCAGCAACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:28 : GAGGCTGTTGCAGCAACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:33 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:35 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:35 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:36 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:37 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH:38 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDH:38 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDH:48 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDH:48 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDH:48 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDH:48 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCA	-	:		•
DMDHH219: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC: DMDHH211: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH221: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH222: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH224: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH225: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH226: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH227: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH228: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH230: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH230: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH231: SAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH231: SAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH231: SAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH232: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH233: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH235: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH236: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH236: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH236: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH237: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: DMDHH239: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH239: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH239: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH239: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH240: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH241: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDHH241: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC: DMDH441: GAGGCTGTTGCAGAC		•		:
DMDHL20 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL21 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL22 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL23 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHL37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHL45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTC	-	:		
DMDHR21 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR22 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCATATCATCAGCAACCGGTCAAC : DMDHR23 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR24 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR26 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCACCAGCAACCGGTCAAC : DMDHR29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR32 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC : DMDHR36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC : DMDHR38 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATCAGCAACCCGGTCAAC : DMDHR36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATCATATCATC	-	:		
DMDH122 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDH123 : GAGGCTGTTGCAGCAACTGCCG	LpMDHk21	:		:
DNDH124 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH125 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH127 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH127 : GAGGCTGTTGCAGAACCAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH128 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH130 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH131 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH132 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH135 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH135 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH135 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH133 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH138 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH138 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH143 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH144 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DNDH145 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : D	pMDHk22	:		:
DMDHK25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCATATCATCAGCAACCGGTCAAC : DMDHK26 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCATATCATCAGCAACCCGGTCAAC : DMDHK28 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCATATCATCAGCAACCCGGTCAAC : DMDHK28 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK29 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK31 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK31 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK31 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK32 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK33 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK34 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK34 : GAGGCTGTTGCAGACACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK36 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCATCAGCAACCCGGTCAAC : DMDHK37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCATCAGCAACCCGGTCAAC : DMDHK38 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCATCAGCAACCCGGTCAAC : DMDHK39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCATCAGACCCGGTCAAC : DMDHK39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTCATCCATATGATCATCAGACCCCGGTCAAC : DMDHK40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK44 : GAGGCTGTTGCAGCAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATACACCAGCCGGTCAAC : DMDHK45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATATCAGCAACCCGGTCAAC : DMDHK45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATATCAGCAACCCGGTCAAC : DMDHK5 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATATCAGCAACCCGGTCAAC :	pMDHk23	:	GAGGCTGTTGC	:
DNDHR26 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATTCATATCATCAGCAACCGGTCAAC : DNDHR27 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATTCATTC	pMDHk24	:	GAGGCTGTTGCAGACAACTGCCC	:
DMDHK27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATTCATATCATCAGCAACCCGGTCAAC : DMDHK28 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATTCATTC	pMDHk25	:		:
pmbhl28 : dagctgttccagacaactgccttaaggccttcatccatatcatcacacaccagtcaac : dagctgttgcagacaactgcctagggccttcatccatatcatcacacaccaggtcaac : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : pmbhl31 : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatcatcatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatcatcatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatcatcatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatcatcatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttcatccatatcatcagcaacccggtcaac : dagctgttgcagacaactgccctgaggccttgaggccttgatcaactagcaaccaggtcaac : daggctgttgcagacaactgccctgaggccttgaggccttgatcaactagaacacaggcaac : daggctgttgcagacaacacacacccgtcaac : daggctgttgcagacaacacacacacccgtgaggccttgagacacacac	pMDHk26	:	GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCAAC	-
DMDHK29: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC DMDHK30: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK32: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK32: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK34: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK34: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK36: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK36: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK36: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATCATCAGCAACCCGGTCAAC GMDHK37: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATTATCATCAGCAACCCGGTCAAC GMDHK39: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATTATCAGCAACCCGGTCAAC GMDHK39: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATTATCAGCAACCCGGTCAAC GMDHK39: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATTATCAGCAACCCGGTCAAC GMDHK39: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTGATCCATATTATCAGCAACCCGGTCAAC GMDHK40: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK41: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK44: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK45: GAGGCTGTTCCACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK45: GAGGCTGTTCCACACACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK45: GAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK46: GAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC GMDHK		:		-
DMDHR31 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHR32 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR33 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHR37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATTATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATTATCAGCAACCCGGTCAAC : DMDHR39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTTCATCCATATTATTATCAGCAACCCGGTCAAC : DMDHR40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : DMDHR44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : DMDHR46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCA		:		:
pmdhk31 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : pmdhk32 : GAGGCTGTTGCAGACAACTGCC		:		:
DMDHk32 : GAGGCTGTTGCAGACAACTGCC DMDHk33 : GAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCGGTCAAC : DMDHk35 : GAGGCTGTTGCAGACACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk36 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk36 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk37 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk39 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCACAGAACCCGGTCAAC : DMDHk39 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk51 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCATATCATCAGCAACCCGGTCAAC : DMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC : DMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCAGCAACCCGGTCAAC : DMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATATCATCACAACCCGGTCAAC : DMDHk53 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCACACCCGGTCAAC : DMDHk54 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCACACCCGGTCAAC : DMDHk64 : GAGGCTGTTGCAGACAACTGCC	-	:		
DMDHk33 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk34 : GAGGCTGTTGCAGAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk38 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk42 : GAGGCTGTTCCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk43 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk51 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAA	,-			•
OMDHK34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK38 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCACAGACACCCGGTCAAC : DMDHK39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTGATCCATATGATCAGAACCCCGGTCAAC : DMDHK41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTGATCCATATGATCAGCAACCCCGGTCAAC : DMDHK41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCCGGTCAAC : DMDHK42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHK45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHK49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK51 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK65 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGCAACCCGGTCAAC : DMDHK66 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTGATCAGC	-	:		
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DMDHk36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk37 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTT_ATCCATATGATCA_MACCCCGGTCAAC : DMDHk38 : GAGGCTGTTGCAGACAACTGCCCTGAGGGCTTGATCCATATGATGAGAAGCCCGGNCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTGATCCATATGATCAGCAACCCGGTCAAC : DMDHk41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : DMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk51 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk51 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk53 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk65 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk66 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMDHk66 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATGATCAGCAACCCGGTCAAC : DMD	-	:		
pmdhk37; gaggctgttgcagac_act_gcctt_atcatat@acat@acatagacacacacacacacacacacacacacacacacac	-			:
pmdhk38 : GAGGCTGTTGCAGACACTGCCCTGAGGNCTTGATCATATHATGAGAACCCGGNCAAC : PMDHk39 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTUTCTGAGACACTGCAACTGCCCTGAGGCCTTCATCATATHATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : CAGGCTGTTGCAGACAACTGCCCTGAGGCCTT	pMDHk37	:	gaggctgttgcagac-act-ecctgaggcctt-atccatatiiatca-nnacccggeac	:
pMDHk40: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk41: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk42: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk43: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk45: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk46: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk46: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk48: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk50: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGAGCAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGAGCAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGACACACTGCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAA	pMDHk38	:	GAGGCTGTTGCAGACAACTGCCCTGAGGÄCTTGATCCATATHATGAGÄÄCCCCGGÑCAAC	:
pMDHk41: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk42: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk44: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk45: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk45: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk46: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk49: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk49: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk50: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk52: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk58: AGGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk59: AGGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGAGCAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGAGCAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGAGCAACTGCCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGACACACTGCCTGAGGCCTTCATCCATAT#ATCAGCAACCCGGTCA	pMDHk39	:		:
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pMDHk49: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk50: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk52: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk53: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk59: AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk66: GAGGCTGTTGATCATATHATCAGCAACCCGGTCAAC: pMDHK66: GAGGCTGTTGATCATATHATCAGCAACCCGGTCAAC: pMDHK66: GAGGCTGTTGATCATATHATCAGCAACCCGGTCAAC: pMDHK66: GAGGCTGTTGATCATTATTATCATCAGCAACCCGGTCAAC: pMDHCATATHATCAGCAAC	pMDHk48	:		
pMDHk50: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk52: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk53: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk59: AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk59: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC: pMDHK66: GAGGCTGTTGATCATCATCATCAGCAACCCGGTCAAC: pMDHK66: GAGGCTGTTGATCATCATCATCATCAGCAACCCGGTCAAC: pMDHK66: pAGGCTTTGATCATCATCATCATCATCAGCAACCCGGTCAAC: pMDHK66: pAGGC	pMDHk49	:		:
pMDHk51: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk52: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk53: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk54: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk59: AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC:	pMDHk50	:	GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT;ATCAGCAACCCGGTCAAC	:
pMDHk53 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk54 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk57 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk58 : pMDHk59 : AGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : pMDHk61 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : pMDHk62 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk63 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : pMDHk66 : GAGGCTGTTGAGCACCCGGTCAAC : pMCHANCACTGCCTGAGGCCTTCATCCATATTATCATCAGCAACCCGGTCAAC : pMCHANCACTGCCTGAGACCCGGTCAAC : pMCHANCACTGCCTGAGACCCGGTCAAC : pMCHANCACTGCCTGAGCCTTCATCATATTATCATCAGCAACCCGGTCAAC : pMCHA	<b>-</b>	:	GAGGCTGÑTGCAGACAACTGCCCTGAGGCCTTCATCCATATÑATCAGCAACCCGGTCÑA	:
pMDHk54 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk56 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk57 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk59 : AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : pMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : pMDHk61 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk63 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk63 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk64 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATÄATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATÃATCATCAGCAACCCGGTCAAC : pMDHLAGACACTGCCCTGAGGCCTTCATCCATATÃATCATCAGCAACCCGGTCAAC : pMDHLAGACACTGCCCTGAGGCCTTCATCCATATÃATCATCAGCAACCCGGTCAAC : pMDHLAGACACTGCCCAGACACTGCCCTGAGGCCTTCATCATCATCATCATATCATCAGCAACTGCCCTGAGACCCCGGTCAAC : pMDHLAGACCCGGTCAAC : pMDHLA	pMDHk52	:	PA I	:
pMDHk55: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC: pMDHk56: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCÄAC: pMDHk59: ÄAGGCTGTTGCAGACAACTGCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC: pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATÜATCAGCAACCCGGTCAAC:	pMDHk53	:		:
pMDHk56: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk57: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk58:	pMDHk54	:		
pMDHk57: GAGGCTG\(\bar{V}\)TGCAGACAACTGCCCTGAGGCCTTCATCCATAT\(\bar{V}\)ATCAGCAACCCGGTC\(\bar{V}\)AC: pMDHk58: pMDHk59: \(\bar{A}\)AGGCTGTTGCAGACAACTGCC\(\bar{V}\)TGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk60: \(\bar{G}\)AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: \(\bar{G}\)AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: pMDHk63: \(\bar{G}\)AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT\(\bar{V}\)ATCAGCAACCCGGTCAAC: pMDHk64: \(\bar{G}\)AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT\(\bar{V}\)ATCAGCAACCCGGTCAAC: pMDHk65: \(\bar{G}\)AGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATAT\(\bar{V}\)ATCAGCAACCCGGTCAAC:	pMDHk55	:		
pMDHk58:  pMDHk59: AGGCTGTTGCAGACAACTGCCUTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC:  pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC:  pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC:  pMDHk62:  pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC:  pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC:  pMDHk65: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC:	<del>-</del>	:		
pMDHk59: AGGCTGTTGCAGACACTGCCATGCGCTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATAATCAGCAACCCGGTCAAC:	_	:	GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATINATCAGCAACCCGGTCNAC	
pMDHk60: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk61: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62:	-	:	tinggerongeron on an a remission man accompany man man accompany accompany	:
pMDHk61: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC: pMDHk62:	-	:		:
pMDHk62:  pMDHk63: GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC:  pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC:  pMDHk65: GAGGCTGTTGCAGACAACTGCCCÄGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC:	-	:		
pMDHk63: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk64: GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC: pMDHk65: GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC:	-	:	GAGGCIGITGCAGACACIGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	
pMDHk64 : GAGGCTGTTGCAGACACTGCCCTGAGGCCTTCATCCATATNATCAGCAACCCGGTCAAC : pMDHk65 : GAGGCTGTTGCAGACACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC :		•	GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATHATCAGCAACCCGGTCAAC	•
pMDHk65 : GAGGCTGTTGCAGACAACTGCCCÄGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC :	-	•		į
pMDHk66 : GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC :	pMDHk65	:	GAGGCTGTTGCAGACAACTGCCCÄGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	:
	LpMDHk66	:	GAGGCTGTTGCAGACAACTGCCCAGAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	:

		* 740 * 760 <b>*</b> 780		
DHk1	:		:	_
LpMDHk2	:			-
LpMDHk3	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	746
LpMDHk4	:	TMCACTGTTMCACTGTGA		692
LpMDHk5	:	TNCACTGTGA		695
LpMDHk6	:	*	•	-
LpMDHk7	:		:	_
LpMDHk8	:		:	_
LpMDHk9	:	TMCACTGTGCCGATTGCTGCTGA	:	706
LpMDHk10	:	TCCACTGTGCCGATTGCTGCTGAA	:	706
LpMDHk11	:	TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCCAAGAAG		741
LpMDHk12	:	TNCACTGTG	•	691
LpMDHk13	:	TNCACTGTGCCGATTGCTGCTGAG	•	705
LpMDHk14	:		•	705
LpMDHk15	:	TCCACTGTGCCGATTGCTGCTGAGAT	•	705
LpMDHk16	:	TNCACTGTGCCGATTGCTGCTGAGATA	•	705 706
LpMDHk17			•	706
LpMDHk18	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	740
LpMDHk19	:	TCCACTEÑGCCGATTGCTGCTGAÑATTCTGAAACAÑAAGGGCGÑÑTACAACCCCAAÑAAG	•	740
LpMDHk20	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAWAAGGGCGTCTACAACCCCCAAWAAG	•	
LpMDHk21		TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	740
LpMDHk22		TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	:	740
LpMDHk23	:	STOP TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TO	•	740
LpMDHk24	:		:	-
LpMDHk25	:	TCCACTGTGCCGATTGCTGCT	:	-
LpMDHk26	:	TNCACTGTGCCGATTGCTGAGATTCTGAAAN	:	698
LpMDHk27		TCCACTGTGCCGATTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	713
LpMDHk28		TCCACTGTGCCGATTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	:	738
LpMDHk29		Tacactgtgc	:	739
LpMDHk30	:	TNCACTGTGCCGATTGA	•	684
LpMDHk31		TNCACTGTGCCGATTGCTG	:	695
LpMDHk32			•	695
LpMDHk33	:		•	-
LpMDHk34		TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGGCGTHT-CEACCCCAAGAAG	•	774
LpMDHk35		TCCACGGTGCCGATTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	734
LpMDHk36	:	TNCACTGTGCCGATTGCTGAGATTCTGAA	•	734
LpMDHk37	:	TGCACGGTGCCGATTGCTGAAA	:	706
LpMDHk38	:	TCCACGGGGCCGATTGNTGCNGAGATTCTGAAACAGAA-GGCGT	•	682 712
LpMDHk39	:		•	112
LpMDHk40	:	TNCACGGTGCCGAT	•	683
LpMDHk41	:	TCCACGGTGCCGATTGCTGCAGAGA	•	695
LpMDHk42	:	TCCACGGTGCCGATTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	•	726
LpMDHk43	:		•	720
LpMDHk44	:	TÄCACTGTGCCGATT	:	686
LpMDHk45	:	TWCACTGTGCCGATTGCTGCTGE	:	693
LpMDHk46	:		:	093
LpMDHk47	:		:	_
LpMDHk48	:		:	-
LpMDHk49	:	TCCACGGTGCCGATTG	:	681
LpMDHk50	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	:	727
LpMDHk51	:	***************************************		-
LpMDHk52	:	TNCACGGTGCCGATN		680
LpMDHk53	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAGAGAG		726
LpMDHk54	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAGGTCTACAACCCCAAGAAGTCCCAAGAAGGTGCGTGC	į	702
LpMDHk55	:	TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG		723
LpMDHk56	:	TÜCACĞGTGCCGATTGCTĞÇAĞAGATTCTGAAACA AAAĞGGCGTCTACAAC	:	707
LpMDHk57	:	TCCACGGÜGCCGATTGÜTGCÄ AÑATTÄTGĞ	:	687
LpMDHk58	:			-
LpMDHk59	:	P(C	:	642
LpMDHk60	:	TÜCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG		702
LpMDHk61	:	TMCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACACCCCCAAGAAG		695
LpMDHk62	:		:	
LpMDHk63		<u>n</u>	:	630
LpMDHk64		TWCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAA		671
LpMDHk65	:	TCCACTGTGCCGATTGCTGAGATTCTGAAACAGAAGGGTGTCTACAACCCCAAGAAG		407
LpMDHk66	:	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGÄGTCTACAACCCCAAGAAG		294

		* 800 * 820 * 840	
MDHk1	:		; -
LpMDHk2	:		: -
LpMDHk3	:	CTCTTCGGGGTTT <u>N</u> CACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANA	: 801
LpMDHk4	:		: -
LpMDHk5	:		: -
LpMDHk6	:		: -
LpMDHk7	:		: -
LpMDHk8	:		: -
LpMDHk9	:		: -
LpMDHk10	:		: -
LpMDHk11 LpMDHk12	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAMAANAAN	: 801
LpMDHk13	•		: -
LpMDHk14	•		: -
LpMDHk15			: -
LpMDHk16	:		: -
LpMDHk17	:	***************************************	: -
LpMDHk18		CTCTTCGGGGTTTCCACC	: 758
LpMDHk19	:	CTCTTMGGGGMTTMCACCCTG	: 761
LpMDHk20	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAA	: 772
LpMDHk21	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAN	: 772
LpMDHk22	;	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAAGAAG	: 800
LpMDHk23	:		: -
LpMDHk24	:	~	: -
LpMDHk25	:		: -
LpMDHk26	:		: -
LpMDHk27	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGA	: 771
LpMDHk28 LpMDHk29	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAG	: 773
LpMDHk30	:		: -
LpMDHk31	:		: -
LpMDHk32	:	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	
LpMDHk33	:		: - · -
LpMDHk34	:	CTHTTCNGGGNTTACACCCTGGATGTTGEC	: 764
LpMDHk35	:	CTCTTCGGGGNTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCT	. 701 : 785
LpMDHk36	:		: -
LpMDHk37	:		· • -
LpMDHk38	:		: -
LpMDHk39	:		: -
LpMDHk40	:	***************************************	: -
LpMDHk41	:		: -
LpMDHk42 LpMDHk43	:	CTCTTCGGGGTTTNCACCCTGGATGTTGTCAGAGCTAACACATTTGNAGCTCANAANAAG	: 786
LpMDHk44	:		: -
LpMDHk45	:		: -
LpMDHk46	:		: - -
LpMDHk47	:		; <del>-</del> 
LpMDHk48	:		
LpMDHk49			· : -
LpMDHk50	:	CTCTTCGGGGTTTC	741
LpMDHk51	:		-
	:		-
LpMDHk53	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGGGCTAACACATT	770
LpMDHk54	2		; <b>-</b>
•	:	CTCTTCGGGGTTTCCGCCCTGGATGTTGTCAGGGCTAACACATTTGTAGCTCA	777
LpMDHk56 LpMDHk57	:		-
LpMDHk58	:		-
•	:		. <b>-</b>
LpMDHk60	-	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	760
LpMDHk61	:	CTCTTA	762
LpMDHk62			,0T
LpMDHk63	:		
LpMDHk64	:		-
LpMDHk65	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	467
LpMDHk66	:	CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG	354

	*	860	*	880	*	900	
EpWDHk1	:						
LpMDHk2	:						•
LpMDHk3	:						
LpMDHk4	:						•
LpMDHk5	:						-
LpMDHk6							: -
LpMDHk7							: -
•							: -
LpMDHk8	:						: -
LpMDHk9							: -
LpMDHk10							: -
LpMDHk11	: A						: 802
LpMDHk12							: -
LpMDHk13							: -
LpMDHk14							: -
LpMDHk15 :							: -
LpMDHk16 :							
LpMDHk17 :							• -
LpMDHk18 :							· · -
LpMDHk19 :							• -
LpMDHk20 :							• -
LpMDHk21						,	-
LoMDHk22	AACCTCA	. <b></b>					: -
LpMDHk23							: 807
LpMDHk24	_						: -
LpMDHk25 :							: -
•							: -
LpMDHk26 :						;	: -
LpMDHk27 :	~~~~~~					;	: -
LpMDHk28 :						;	: -
LpMDHk29 :	*						: -
LpMDHk3.0 :						;	: -
LpMDHk31 :							: -
LpMDHk32 :						;	: -
LpMDHk33 :						;	: -
LpMDHk34 :						;	
LpMDHk35 :						;	: -
LpMDHk36 :						;	: -
LpMDHk37 :						;	: -
LpMDHk38 :						;	-
LpMDHk39 :							_
LpMDHk40 :							
LpMDHk41 :						1	_
LpMDHk42 :	AACCTCAGHCTHATC	<b>6</b>				:	802
LpMDHk43 :							
LpMDHk44:							_
LpMDHk45 :							_
LpMDHk46:							-
LpMDHk47:							_
LpMDHk48 :							-
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LpMDHk50 :						:	-
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LpMDHk54 :							-
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LpMDHk56 :							-
						:	-
LpMDHk57 :						:	-
LpMDHk58 :						:	-
LpMDHk59 :							-
LpMDHk60:	AACCT						767
LpMDHk61:						:	-
LpMDHk62:					,	:	-
LpMDHk63:						:	-
LpMDHk64:						;	-
LpMDHk65:	AACCTCAGCCTCATC	GATGTTGATO	STCCCAGTTGT	CGGTGGCCA	TGCTGGGATC	ACGATT :	527
LpMDHk66:	AACCTCAGCCTCATC	GATGTTGATO	TCCCAGTTGT	CGGTGGCCA	TGCTGGGATC	ACGATT :	414

		*	920	*	940	. + 00	^
=pWDHk1	:					· * 96	U
LpMDHk2	:						- :
LpMDHk3	:						- :
LpMDHk4	:						- :
LpMDHk5	:						- : - :
LpMDHk6	:						- :
LpMDHk7	:						- :
LpMDHk8	:						
LpMDHk9	:						<b>-</b> :
LpMDHk10	:						• :
LpMDHk11	:						- :
LpMDHk12	:						- :
LpMDHk13	:						• :
LpMDHk14	:						• :
LpMDHk15	:						• :
LpMDHk16	:						• •
LpMDHk17	:						• :
LpMDHk18	:						•
LpMDHk19	:						, <b>:</b>
LpMDHk20	:						• •
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LpMDHk24	:						:
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LpMDHk31	:						:
LpMDHk32	:					,	•
LpMDHk33	:		· • • • • • • • • • • • • • • • • • • •				•
LpMDHk34	:						•
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LpMDHk60:							<u> </u>
LpMDHk61 :							· -
LpMDHk62:							-
LpMDHk63 :							-
LpMDHk64:							
LpMDHk65:	CTGCCT	CTGTTGT	CCAAGACTAGG	CCTTCTGTCA	GCTTCACGC	ACGAGGAAACTGAACAG	: - : 587
LpMDHk66:	CTGCCT	CTGTTGT	CCAAGACTAGG	CCTTCTGTCA	GCTTCACGG	ACGAGGAAACTGAACAG ACGAGGAAACTGAACAG	: 474

DVII-4		*	;	980	*	1000	<b>*</b>	1020	_	
LpMDHk2	:							. <b></b>	:	-
LpMDHk3									•	_
LpMDHk4	:								:	-
LpMDHk5	:								:	_
LpMDHk6	:								:	-
LpMDHk7	:								:	-
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LpMDHk10	:								:	-
LpMDHk11	:								:	-
LpMDHk12	:								:	-
LpMDHk13	:								:	-
LpMDHk14	:								:	-
LpMDHk15	:								:	_
LpMDHk16 LpMDHk17	:								:	_
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LpMDHk22	:								:	-
LpMDHk23	:								:	-
LpMDHk24	:								:	-
LpMDHk25	:								:	-
LpMDHk26	:								:	-
LpMDHk27	:								:	<u>-</u>
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LpMDHk30	:									_
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LpMDHk36	:							· <b></b>	:	-
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LpMDHk40 LpMDHk41	:								:	_
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LpMDHk58	:								:	-
LpMDHk59	:								:	-
LpMDHk60	:								:	-
LpMDHk61	:								:	-
LpMDHk62 LpMDHk63	:								•	-
LpMDHk64	:								•	
LpMDHk65	:	CTGACAAAGAG	GATACA			GTGGAGGCGAA-			:	634
LpMDHk66	:	CTGACAAAGAG	GATACA	GAACGCTGGGAC	AGAGGCG	GTGGAGGCGAAG	GCTGGTGC	TGGC	:	534

	*	1040	*	1060 ·		
JANDHk1	:			1080 .	<b></b>	1080
LpMDHk2	:					:
LpMDHk3	:					:
LpMDHk4	:					:
LpMDHk5			~			:
LpMDHk6						:
	:					
LpMDHk7	:					
LpMDHk8	:					:
LpMDHk9	:					
LpMDHk10	:					:
LpMDHk11	:					:
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LpMDHk58 :	***************************************					: -
LpMDHk59						: -
LpMDHk60 :						: -
LpMDHk61 :						: -
LpMDHk62:						: -
LpMDHk63						<u> </u>
LpMDHk64:						
						:
LpMDHk65 : -						
LpMDHk66 :	CTGCTACTCTGTCCAT	GGCTTATGC	CGCTGCCAGAT	TTGTTGACT	CATCCCTCCCCC	
					G-11 CGC 1 CCGCG(	ZA : 594

		*	1100	*	1120	*	1140	
_pMDHk1	:							: -
LpMDHk2	:							: -
LpMDHk3	:							: -
LpMDHk4	:							: -
LpMDHk5	:							: -
LpMDHk6	:							: -
LpMDHk7	:							: -
LpMDHk8	:							: -
LpMDHk9	:							: -
LpMDHk10	:							: -
LpMDHk11	:							: -
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LpMDHk58	:							
LpMDHk59	:							: -
LpMDHk60								-
LpMDHk61								: -
LpMDHk62	•							<del>-</del>
LpMDHk63	:							
LpMDHk64	:							· -
LpMDHk65	:							· -
	:	ATGGCTGGTGATCCAG	ATGTTTACGAGTC	САССТАТ	СТТСАСТСТЕЛС	TTAACACA	GCTT	: - : 654
_					ONG LC LONG		للتنب	. 554

		•	*	1160	*	1180	*	1200	
PMDHk1						· <del>·</del>			:
LpMDHk2		:							:
LpMDHk3		:							:
LpMDHk4									:
LpMDHk5									
LpMDHk6	:								•
LpMDHk7	:								:
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LpMDHk10	:								•
LpMDHk11	:								:
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LpMDHk16	:								•
LpMDHk17	:								•
LpMDHk18	:								•
LpMDHk19	:								:
LpMDHk20	:								•
LpMDHk21	:								•
LpMDHk22	:								•
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LpMDHk25	:								•
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LpMDHk27	:								:
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LpMDHk60	:								: -
LpMDHk61	:								: -
LpMDHk62	:								: -
LpMDHk63	:								: -
LpMDHk64	:								: -
LpMDHk65	:	COMPRESS							: -
LpMDHk66	:	CCATTCT	ICGCGTCCA	GAGTTAAGCT	TGGGAAGG	CGGNGTTGAGT	CCATCATTT	CCTCC	: 714

		*	1220		*	1240	*	1260	
Hk1	:								•
LpMDHk2	:								:
LpMDHk3	:								
LpMDHk4	:								:
LpMDHk5	:								•
LpMDHk6	:								:
LpMDHk7	:								•
LpMDHk8	:								•
LpMDHk9	:								:
LpMDHk10	:						:		
LpMDHk11	:								•
LpMDHk12	:								•
LpMDHk13	:			,					
LpMDHk14	:								•
LpMDHk15	:								
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LpMDHk37	:							:	-
LpMDHk38	:							:	-
LpMDHk39	:							:	-
LpMDHk40	:							:	-
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LpMDHk62 :									_
LpMDHk63:								:	_
LpMDHk64:									-
LpMDHk65 :									-
LpMDHk66:		GACCTGGAGGGAGTGA	CGGAGTAC	GAGGCCA	AGGC	CGCTTGANGCA	TTGAAGGCTG.	AGCTG:	774

J.

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							•			
fik1				_						
LpMDHk2	:		:	_						
LpMDHk3	:		:	-				•		
LpMDHk4	:		:	-			•			
LpMDHk5 LpMDHk6	:		:	-					•	
LpMDHk7	:		:	-						
LpMDHk8	:	~	:	-						
LpMDHk9 LpMDHk10	-		:	-					•	
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LpMDHk15	:		:	-						
LpMDHk16			:	-						
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LpMDHk19	:		:	-		•				
LpMDHk20			:	-						
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LpMDHk23	:		:	-	•					
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LpMDHk34			:	_						
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LpMDHk61	:		:	-						
LpMDHk62 LpMDHk63				_						
LpMDHk64	:		:	_						
LpMDHk65	:		:	-				. •		
LpMDHk66	:	AAG	: 7	7 <b>7</b>				•		

LpMDHl	:	* 20 * 40 * 60 GNAAACAGNNGCGNCTTTTCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA		60
			•	0.
T MD-1177		*. 80 * 100 * 120		
THUMIT	:	TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCTGGTA	:	120
		* 140 * 160 * 180		
LpMDHl	:	CGTTTGATGTATTAGTGATGCCAAATCTATATGGCGACATTATTAGTGATCTATGTGCTG	:	180
LpMDH1	:	* 200 * 220 * 240 GTTTGATCGGAGGTTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTTGTC	:	240
LpMDHl		* 260 * 280 * 300		
	•	TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGACCTGGCAAACCCAA	:	300
		* 320 * 340 * 360		
LpMDH1	:	CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCGCCACTTGCAATTNAACGACCAAGCAN	:	360
f vicing a		* 380 * 400 *		
LPMDH1	:	AACGGATCCACAATGCTATCCTCCAGACTATCGNCGAGGGGAAGNACANAACTG : 414		

# re 39 Deduced amino acid sequence of LpMDHl

\* 20 \* 40 \* 60

LpMDHl: KQXXLFXXCCRAIAXKYPEIIYEEVIIDNCCMTLVKNPGTFDVLVMPNLYGDIISDLCAG: 60

80 100

LpMDH1 : LIGGLGLTPSCNIGEGGICLAEAVHGSAPDISGKNLANPTALMLSAVMMLRHLQXNDQAX : 120

LpMDH1 : RIHNAILQTIXEGKXXT : 137

LpMDHm	:	* 20 * 40 * 60 GNCACCNCCAGNNACAACTCTGGTACCTCAATTGCTACTCCACACCTCACTACTTCTACC	:	60
LpMDHm	:	*` 80 * 100 * 120 AATCCACTACACAGCTTCGAGCTACCCCGCCCCGCAATCCAAACTACCTCTCCCTAGCA	:	120
LpMDHm	:	* 140 * 160 * 180 AATCTACAACATGAAGGCAGTCGTAGCTGGAGCCGCCGGTGGCATTGGACAGCCATTGTC	:	180
LpMDHm	:	* 200 * 220 * 240 CCTCCTCCTTAAGACCTGCCCGCTCGTCACTGAGCTCGCCCTATACGATGTCGTCAACGC .	:	240
LpMDHm	:	* 260 * 280 * 300 CGTCGGTGTCGCGACTGACCTCTCCCACATCTCCTCGCCCGCGAAAGTAACCGGCTACCT	:	300
LpMDHm	:	* 320 * 340 * 360 GCCGGCAAATGACGGTATGCAGCAGGCTCTCACTGGCGCCGACATCGTGGTCATCCCCGC	:	360
LpMDHm	:	* 380 * 400 * 420 TGGTATTCCCCGCAAGCCCGGCATGACCGTGACGACCTCTTCAAGATCAACGCCGGCAT	:	420
LpMDHm	:	* 440 * 460 * 480 TGTCCAGGGTCTCATCGAGGGTGTCGCCAAGCACTGCCCCAAGGCATACGTTCTCGTCAT	:	480
LpMDHm	:	* 500 * 520 * 540 CTCCAACCCCGTCAACTCGACTGTGCCCATCGCCGCGAGGTGCTGAAGAAGGCCGGTGT	:	540
LpMDHm	:	* 560 * 580 * 600 CTTCGACCCCAAGAAGCTCTTCGGTGTCACCACCCTCGATGTCGTCCGCGCCGAGACCTT	:	600
LpMDHm	:	* 620 * 640 * CGTTGCCGAGATCACTGGCGAGAGGACCCCAGCGAAGTTGAACATNCCCGTA : 652		

\* 20 \* 40 \* 60

LpMDHm : XXPXTTLVPQLLLHTSLLLPIHYTASSYPAPAIQTTSP\*QIYNMKAVVAGAAGGIGQPLS : 59

\* 80 \* 100 \* 120

LpMDHm : LLLKTCPLVTELALYDVVNAVGVATDLSHISSPAKVTGYLPANDGMQQALTGADIVVIPA : 119

\* 140 \* 160 \* 180

LpMDHm : GIPRKPGMTRDDLFKINAGIVQGLIEGVAKHCPKAYVLVISNPVNSTVPIAAEVLKKAGV : 179

\* 200 \*

LpMDHm : FDPKKLFGVTTLDVVRAETFVAEITGEKDPAKLNXPV : 216

LpPEPCa :	* 20 GNGTACACGAAATAGAATCAA	* ACGGAAAGCANGAAGTGAT		
-				
LpPEPCa :	* 80 GAAGGATGCTGGCCGTTTCTC	* 10° CTGCTGGTTGGCACTTGTA		
_				
LpPEPCa :	* 140 TAAGGTTGCGGAGACGTTTGC	* 16 GGGTTAAGNTGACTATGTT		
		-		
LpPEPCa :	* 200 TGGAAGAGGTGGCGGCCCTAG	22 CCCATCTTGCTATACTGTC		
				•
LpPEPCa :	* 260 TGGATCACTTCGGGTAACTG	* 28 TTCAAGGTGAAGTCATTGA		
	* 320	* 34	0 * 36	0
LpPEPCa :	TTTGTGTTTTAGAACGCTTC			
	* 380	* 40	0 * 42	0
LpPEPCa :	ACCAATCTCACCTAAACCAGA	ATGGCGTGCTTTGATGGA	TGAAATGGCTGTTGTTGCCA	C : 420
T	* . 440	* 46		•
прикиса :	AGAGGAATACCGTTCCATTG	rrirccaagaaccaagatri	rgrigagrafficegeerig	C : 480
· LpPEPCa :	* 500 AACACCAGAGCTCGAGTATG	* 52 Saaddtaaraadaaca		
_p · ·				
LpPEPCa :	* 560 AAGCGGAGGAATCGAATCATT	* 58 GCGTGCAATTCCTTGGAT		
LpPEPCa :	* 620 ATTCCACCTGCCAGTGTGGCT	* 64 TTGNTTTTGGTGCGGCCTT		_
	+ 600	+ · · 70	o + 73	^
LpPEPCa :	* 680 CATTCGTANTCTTCAAATCCT		-	
	* 740	* 76	0	
LpPEPCa :	AAACCTGGTTGAGATGGTGTT	•	-	

\* 20 \* 40 \* 60

LpPEPCa : XTRNRINGKXEVMIGYQHSGKDAGRFSAGWHLYKAQBELIKVAETFGVKXTMFHGRGGTV : 60

\* 80 \* 100 \* 120

LpPEPCa : GRGGGPTHLAILSQPPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHP : 120

LpPEPCa : PISPKPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSRPSKRKP : 180

\* 200 \* 220 \* 240

LpPEPCa : SGGIESLRAIPWIFAWTQTRFHLPVWLXFGAAFKHVLQKDIRXLQILQQMYNEWPFRVTI : 240

LpPEPCa : NLVEMVFAKGDPGIAA : 256

: 60	60 TTGTT	* AGAGCTCCCAGCA	40 TGTCCTTGCA	* AGNACATTIN	20 TGATGTTTTA	* GAAGAAGTTGC	:	LpPEPCb
: 126	120 GCTTT	* TGTGCTTGCTGTT	100 CCCATCTGATO	* TGGCAACTGC	80 AASTSTAST	* TTGGTGCTTAC	:	LpPEPCb
: 180	180 GCTTG	* FCCACTATTTGAA	160 GAGAGTTGTTC	* AAAAGCCATT	140 GCCATATAA	* TGCAGCGGGAG	:	Lppepcb
240	240 CATGA	* FTCAATAGACTGG	220 ACGACTATTT	* CATCTGTTGC	200 ICAGCTCCAG	* CAGATCTTGAAI	:	LpPEPCb
300	300 CGCTG	* AGACTCTGGGAAGG	280 IGGATACTCAG	* AGGTCATGAT	260 GCAAGCAGG	* ATAGAATCAAT	:	LpPEPCb
360	360 GGCAA	* AGATCTCATAAAGO	340 AGCACAAGAAG	* AAATGTATAA?	320 CAGCGTGGC	* GGCGTCTCTCT(	:	LpPEPCb
420	420 AGGAG	* PGGAACGGTTGGCA	400 rggaagaggtg	* CAATGTTTCA:	380 TAAAGTTAAA	* AGCAATATGGAC	:	LpPEPCb
480	480 ACTTC	* ACGATACAAGGAT	460 ACCACCAGACA	* FATTATCTCA <i>F</i>	440 ATCTTGCTA	* GTGGTCCCAGTC	:	LpPEPCb
540	540 CTTCA	* .GAGGAACACTTGT	520 CTCATTTGGAG	* CCATAGAGCAC	500 AAGGCGAGGT	· GTGTAACAGTTC	:	LpPEPCb
600	600 TCAC	* ATGCATCCTCCAA	580 GAGCATGGAA	* CAGCTACTCTT	560 GTTTCACTGO	* GAACTCTGCAAC	:	LpPEPCb
660	660 TATC:	* GTGGCAACAAAAG	640 ATGGCTGTAG	* CAATGGATGAG	620 GGCGTGCTAT	CCAAGCCAGAAT	:	LpPEPCb
720	720 'GAGA :	* CGCTCGGCAACAC	700 GAATACTTCC	* ACGTTTTGTC	680 ICCAAGAACC	* SATCAATTGTCT	:	LpPEPCb
780	780 GGCA :	* AGAAAGCCTAGTG	760 CCATCAAAGAG	* TGGTAGCCGG	740 GATGAATAT	* CTGAATATGGTC	:	LpPEPCb
840	840 CTTC :	* CAGACAAGGTTTC	820 GCTTGGACACA	* ATGGATCTTT	800 STGCAATTCC	* PAGAATCGCTCC	:	LpPEPCb
900	900 AATA :	* CAGAAGGACATCA(	880 CATATCATGCA	* AGCGTTCAAA	860 SATTTGGTGC	* CTGTATGGCTTG	: 1	LpPEPCb
960	960 TTGC :	* AGGGTCACCCTTG&	940 CCATTCTTAG		920 AGAAATGTA	* CCATACTCTGA	: '	LpPEPCb

PPCb : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 1020 LpPEPCb : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 1080 LPPEPCb : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 1140 LpPEPCb : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCNACACCC : 1200 LpPEPCb : TGAAGCGGATAAGAGCCCTAGCTTCGAGGTGACACCGCAGCAGCACCTCTGTCGAAGG : 1260 LpPEPCb : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 1320 LPPEPCb : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 1380 LPPEPCb : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGATGGGGCGTGA : 1440 LpPEPCb : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 1500 LpPEPCb : TTGGTTATGGATGNACTTTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 1560 LPPEPCb : ATATGGAACAATGATATTCTGGTNGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 1620 

LpPEPCb : GNGATTTGGAGTNGTTTAAC : 1640

		* 20 * 40 *	60		
LpPEPCb	:	RSCXCFKXIXVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKKPLRVVPLFE	KLA	:	60
		* 80 * 100 *	120		
LpPEPCb	:	DLEXAPASVARLFSIDWYMNRINGKQEVMIGYSDSGKDAGRLSAAWQMYKAQEDLIR	CVAK	:	120
_		•			
		* 140 * 160 *	180		
I NDEDCH		QYGVKLTMFHGRGGTVGRGGGPSHLAILSQPPDTIQGSLRVTVQGEVIEHSFGEEHI		:	180
превесь	•	\$10.101111111010011.0000101111110\$11511\$-0-11111			
			0 4 Å		
		* 200 * 220 *	240		240
LpPEPCb	:	TLQRFTAATLEHGMHPPISPKPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSAT	LPDI	•	240
		* 260 * <sup>'</sup> 280 *	300		
LpPEPCb	:	EYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKD	ERNI	:	300
		,			
		* 320 * 340 *	360		
LpPEPCb	:	HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSEDLQPFGEQLRNNFE	ETKQ	:	360
		·			
		* 380 * 400 *	420		
LpPEPCb	:	LLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPI	LSKE	:	420
•					
		* 440 * 460			
LpPEPCb	:	FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG: 462			

ure 46 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpPEPCb

LpPEPCb1	* 20 * 40 * 60  GAAGAAGTTGCTGATGTTTTAAGNACATTTNTCTCCTTCCACACGTGCACGT		
		:	60
LpPEPCb2		:	_
LpPEPCb3		:	_
LpPEPCb4	:		_
LpPEPCb5		•	
LpPEPCb6		:	-
-F- 21 02 0		:	_
	* 80 * 100 * 120		
LpPEPCb1	TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCT		120
LpPEPCb2			120
LpPEPCb3		•	-
LpPEPCb4		:	-
LpPEPCb5		:	-
LpPEPCb6		:	-
mpr br CDO		:	-
	* 140 * 160 * 180		
LpPEPCb1 :	TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCCTTG		180
LpPEPCb2 :		•	100
LpPEPCb3 :		:	-
LpPEPCb4 :		:	-
LpPEPCb5		:	-
LpPEPCb6:		:	-
nprercne :		:	-
	* 200 * 220 * 240		
LpPEPCb1 :	CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA		240
LpPEPCb2 :		•	240
LpPEPCb3 :		:	-
LpPEPCb4 :		:	-
LpPEPCb5 :		:	-
LpPEPCb6 :		:	-
uprercue :		:	-
	·		
	<u>* 260</u> * 280 * 300		
LpPEPCb1 :	ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG		300
LpPEPCb2 :		•	500
LpPEPCb3 :		•	_
LpPEPCb4 :		:	-
LpPEPCb5 :		:	-
LpPEPCb6 :		:	-
HPFEFCD6 :		:	-
	·		
	* 320 * 340 * 360		
LpPEPCb1 :	GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA		360
LpPEPCb2 :	GTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA	•	
LpPEPCb3 :	O MINIMOCACAMORAGATCICATAMAGGIGGCAA	:	35
LpPEPCb4 :	***************************************	:	-
LpPEPCb5 :		:	-
LpPEPCb6:		:	-
ייף פער ארם יי		:	-
	•		
	* 380 * 400 * 420		
LpPEPCb1 :	AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG		
LpPEPCb2 :	AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG	. 4	120
LpPEPCb3 :	A AUGUSTA DE LA CONTROL DE LA	:	95
LpPEPCb4 :	AATGTTT - NTGGAAGAGTGGAACGGTTGGCAGAGGAG	:	37
LpPEPCb5 :	GCAÑAGGAG :	:	9
		;	-
LpPEPCb6 :		;	-

	* 440 * 460 * 480		
LpPEPCb1 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC	: 480	
LpPEPCb2 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC	: 155	
LpPEPCb3 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACHAGACACGATACAAGGATCACTTC	: 97	
LpPEPCb4 :	GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC	: 69	
LpPEPCb5 :	O TO TECHNOLIST TO THE TECHNOLIST THE TOTAL THE TECHNOLIST THE TEC	. 05	
LpPEPCb6 :		•	
DELLICES .		•	
	* 500 * 520 * 540		
LpPEPCb1 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA	: 540	
LpPEPCb2 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGGGGAACACTTGTGCTTCA	: 215	
LpPEPCb3 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA	: 157	
LpPEPCb4 :	GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA	: 129	
LpPEPCb5 :	CTC TITLE CONTROL CALLACACE CALL TO CONTROL CALL TO TOC TICK	. 127	
LpPEPCb6 :		: -	
	,	•	
	* 560 * 580 * 600		
LpPEPCb1 :	MAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCCC	: 600	
LpPEPCb2 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC	: 275	
LpPEPCb3 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC	: 217	
LpPEPCb4 :	GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC	: 189	
LpPEPCb5 :		:	•
LpPEPCb6 :		· -	
•		•	
	* 620 * 640 * 660		
LpPEPCb1 :	CCAAMCCAGAATGGCNTGCTATAATGGATGANATGGCTGTAGNGGCAGCAAAAGAAMATC	: 660	
LpPEPCb2 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC	: 335	
LpPEPCb3 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC	: 277	
LpPEPCb4 :	CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC	: 249	
LpPEPCb5:		: -	
LpPEPCb6 :		: - '	
(0)	<u>* 680 * 700 * 720</u>		
LpPEPCb1 :	GATCAATTGNCTTCCAAGAACCGCNTTTTGNCNAATA	: 697	
LpPEPCb2:	GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA	: 395	
LpPEPCb3:	GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA	: 337	
LpPEPCb4 :	GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA	: 309	
LpPEPCb5 :		: -	
LpPEPCb6:	7	: -	•
	•		
	* 740 * 760 * 780		
LpPEPCb1 :	* 740 * 760 * 780		
LpPEPCb2 :	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA	: 455	
LpPEPCb3:	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA	: 455	
LpPEPCb4 :	CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA	: 369	
LpPEPCb5 :	DI DOS MONTONIO IL LIGO MONTONIO IL LIGIDIO DE LA CONTROL	. 505	
LpPEPCb6:			
	* · 800		
LpPEPCb1 :	U2V " U2V	: -	
LpPEPCb2 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC	: 515	
LpPEPCb3 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC	: 457	
LpPEPCb4 :	TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC	: 429	
LpPEPCb5 :		: -	
LpPEPCb6 :		: -	

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LpPEPCb1								
			•					
		*	860	*	880	*	900	
	:							: -
	: C1	GTATGGCTTG	GATTTGGTGCAG	CGTTCAAAC	ATATCATGCA	GAAGGACATC	AGGAATA	: 575
LpPEPCb3	: C'I	GTATGGCTTG	GATTTGGTGCAG	CGTTCAAAC	ATATCATGCA	GAAGGACATC	AGGAATA	: 517
LpPEPCb4	: CT	GTATGGCTTG	GATTTGGTGCAG	CGTTCAAAC	ATATCATGCA	GAAGGACATC	AGGAATA	: 489
LpPEPCb5	:							: -
LpPEPCb6	:			:				: -
		•	920		040			
LpPEPCb1	:		<i></i>		940	*	960	
LpPEPCb2	: TC	CATACTCTGA	AAGAAATGTACA	ATGAGTGGC	CATTCTTAC	COTON COCOTO	CACTECC	: 635
LpPEPCb3	TC	СВТВСТСТСВ	AAGAAATGTACA	ATGACTEGE ATGACTEGE		CTCACCCIIC	SACTIGC	-
LpPEPCb4	TC	СУТУСТСТСУ	AAGAAATGTACAA	ATGAGIGGC	CATICITIAGO	GICACCCTIC	SACTIGO	: 577
LpPEPCb5		CHINCICION	MOMMATGIACA	AIGAGIGGC	CALICITIAGO	3G1CACCCT1C	SACT I.GC	: 549
LpPEPCb6								: -
2pi Br Cb0								: -
LpPEPCb1		*	980	*	1000	*	1020	
LpPEPCb1	rala-r	CACATGGGGG		magness				: -
-	112	CACATGGTTT	TTGCCAAGGGAGA	ATCCAGGAA	TIGCIGCTTI	YTATGACAAAT	MECTIC	: 695
LpPEPCb3	1101	CACAMOGRAP	TTGCCAAGGGAGA	VICCAGGGA	TIGCTGCTTT/	ATATGACAAA1	TGCTTG	: 637
LpPEPCb4		SAGAT GGTTT	TGCCGAGGAG	ALCCAGGAA	HIGGIGGITTI)	YIATGACAAAT	TGCTTG	: 609
LpPEPCb5	:		TTG-CXAGGGAGA	ATCC-GG-A	TTGCTGCTTT	TATGACAAAT	TGCTTG	: 50
LpPEPCb6	:							: -
		*	1040	* .	1060	*	1080	
LpPEPCb1	:							
LpPEPCb2	: IG	TCTGAAGATCT	GCAGCCCTTTGC	GGAGCAGC	TGAMAAACAAC	TTTCAACACA	CGAAAC	: 755
LpPEPCb3	: TVC	TCTGAAGATCT	GCAGCCCTTTGC	GGAGCAGC	IGVGVVVCVVC	TIIIGAAGAGA	CCAAAC	: 733
LpPEPCb4	. irei	тстсавсатст	GCAGCCCTTTGG	CCACCACC	TO NO A A O A A C	I I I GAAGAGA	CGAAAC	
LpPEPCb5	TC	TCTGAAGATCT	GCAGCCCTTTGG	CCACCATCC	IGAGAAACAAC	TTTGAAGAGA	CGAAAC	: 669
LpPEPCb6		I.C. CAMORICI	GCAGCCCIIIGG	OSMOCINGO	IGAGAAACAAC	TTTGAAGAGA	CGAAAC	: 110
								: -
I m DDDOb 1		*	1100	*	1120	*	1140	
LpPEPCb1 :		*		*	1120	*	1140	: -
LpPEPCb2 :	AGI	TACTCITTÀLA	GGTTGIJTGNCCA	* CAAGG		*		: - : 785
LpPEPCb2 :	: AGT	TTACTCCTTCA	АООЙОТІЙОТТОР <i>.</i> АООООТОТТОР <i>.</i>	CAAGGACG	TCTTGAAGGG	* GAICCTTACC	TGAAGC	757
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 :	AGT	TTACTCCTTCA TTACTCCTTCA	ACCETTGETGE ACCECTGETGE ACCECTGETGETGE	CAAGGACG'	TCTTGAAGGG	GATCCTTACC	TGAAGC	757 729
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 :	AGT AGT	TTACTCCTTCA TTACTCCTTCA	АООЙОТІЙОТТОР <i>.</i> АООООТОТТОР <i>.</i>	CAAGGACG CAAGGACG CAAGGACG	ftcttgaaggg ftcttgaggg ftcttgaaggg	GATCCTTACC GATCCTTACC	TGAAGC TGAAGC	757 729 170
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 :	AGT AGT	TTACTCCTTCA TTACTCCTTCA	ACCETTGETGE ACCECTGETGE ACCECTGETGETGE	CAAGGACG CAAGGACG CAAGGACG	TCTTGAAGGG	GATCCTTACC GATCCTTACC	TGAAGC TGAAGC	757 729
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 :	AGT AGT	TTACTCCTTCA TTACTCCTTCA	ACCETTGETGE ACCECTGETGE ACCECTGETGETGE	CAAGGACG CAAGGACG CAAGGACG	ftcttgaaggg ftcttgaggg ftcttgaaggg	GATCCTTACC GATCCTTACC	TGAAGC TGAAGC	757 729 170
LpPEPCb2: LpPEPCb4: LpPEPCb5: LpPEPCb6:	AGT AGT AGT	TTACTCCTTCA TTACTCCTTCA	ACCETTGETGE ACCECTGETGE ACCECTGETGETGE	CAAGGACG CAAGGACG CAAGGACG	ftcttgaaggg ftcttgaggg ftcttgaaggg	GATCCTTACC GATCCTTACC	TGAAGC TGAAGC	757 729 170
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb6 :	AGT	FTACTCCTTCA FTACTCCTTCA FTACTCCTTCA	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA	CAAGGACG' CAAGGACG' CAAGGACG' GGACG'	FTCTTGAAGGG FTCTTGAEGGG FTCTTGAAGGG FTCTTGAAGGG	GATCCTTACC GATCCTTACC GATCCTTACC	TGAAGC TGAAGC TGAAGC TGAAGC	757 729 170
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb6 : LpPEPCb1 : LpPEPCb2 :	AGT AGT	TTACTCCTTCA TTACTCCTTCA TTACTCCTTCA *	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA	CAAGGACG' CAAGGACG' CAAGGACG'GGACG'	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG	GATOCTTACO GATOCTTACO GATOCTTACO *	TGAAGC TGAAGC TGAAGC TGAAGC	757 729 170 32
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 :	AGT	TTACTCCTTCA TTACTCCTTCA  *  CGTCTGCGGGT	AGGTTGIJTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA 1160	CAAGGACG' CAAGGACG'GGACG'  *	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG	GATOCTTACO GATOCTTACO GATOCTTACO *	TGAAGC TGAAGC TGAAGC TGAAGC	757 729
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 :	AGI AGI AGI AGI AGI AGI AGGI AGGI AGGI	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA  1160 AGGTGAGTCATA	CAAGGACG' CAAGGACG'GGACG'  * CAAGGACG' CAAGGACG' CATCACAA	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG	GATCCTTACC GATCCTTACC GATCCTTACC *	TGAAGC TGAAGC TGAAGC TGAAGC	757 729 170 32
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 :	AGT AGT AGT AGT AGC AGC AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG'GGACG'  * CAAGGACG' CAAGGACG' CATCACAAC	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG 1180	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCCN	TGAAGC TGAAGC TGAAGC 1200	757 729 170 32
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 :	AGT AGT AGT AGT AGC AGC AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG'GGACG'  * CAAGGACG' CAAGGACG' CATCACAAC	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG 1180	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCCN	TGAAGC TGAAGC TGAAGC 1200	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 :	AGT AGT AGT AGT AGC AGC AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGIJTGIJCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA  1160 AGGTGAGTCATA	CAAGGACG' CAAGGACG'GGACG'  * CAAGGACG' CAAGGACG' CATCACAAC	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG 1180	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCCN	TGAAGC TGAAGC TGAAGC 1200	757 729 170 32
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 :	AGT AGT AGT AGT AGC AGC AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGHTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG'GGACG'  * CAAGGACG' CAAGGACG' CATCACAAC	FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG CATTGAATGTT CATTGAATGTT	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCCN	TGAAGC TGAAGC TGAAGC TGAAGC ACACCC	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 :  LpPEPCb1 : LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb6 :	AGT AGT AGT AGT AGC AGC AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGTT CGTCTGCGGGTT CGTCTGCGGGTT	AGGTTGIJTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG' CAAGGACG'  * CAAGGACG' CATCACAACCATCACAACCATCACAACCAACCAACCAAC	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG  ATTGAATGTT FATTGAATGTT	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCCN	TGAAGC TGAAGC TGAAGC 1200	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 :  LpPEPCb1 : LpPEPCb1 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 :	FIDA :	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGT CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT	AGGTTGITGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG' CAAGGACG'  * CAAGGACG' CATCACAAC CATCACAAC	FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG 1180  CA- CATTGAATGTT CATTGAATGTT	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCC TGCCAAGCC  *	TGAAGC TGAAGC TGAAGC TGAAGC ACACCC	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 :  LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb6 :  LpPEPCb6 :  LpPEPCb6 :	FIDA :	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGT CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT	AGGTTGIJTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG' CAAGGACG'  * CAAGGACG' CATCACAAC CATCACAAC	FTCTTGAAGGG FTCTTGAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG  1180  CA	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCC TGCCAAGCC  *	TGAAGC TGAAGC TGAAGC TGAAGC ACACCC	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 : LpPEPCb1 : LpPEPCb1 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 : LpPEPCb5 : LpPEPCb5 : LpPEPCb6 :	FIDA :	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGGT CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT	AGGTTGHTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG' CAAGGACG'  *  CAAGGACG'  CATCACAAC CATCACAAC	FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG 1180  A	GATCCTTACC GATCCTTACC  *  *  TGCCAAGCC TGCCAAGCC  *	TGAAGC TGAAGC TGAAGC TGAAGC ACACCC	757 729 170 32 32 783 764 230
LpPEPCb2 : LpPEPCb3 : LpPEPCb4 : LpPEPCb5 : LpPEPCb6 :  LpPEPCb1 : LpPEPCb2 : LpPEPCb3 : LpPEPCb3 : LpPEPCb4 : LpPEPCb6 :  LpPEPCb6 :  LpPEPCb6 :	AGC	TTACTCCTTCA TTACTCCTTCA  * CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT CGTCTGCGGTT	AGGTTGHTGNCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGGTTGCTGGCCA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA AGCGTGAGTCATA	CAAGGACG' CAAGGACG' CAAGGACG'  * CAAGGACG' CATCACAAC CATCACAAC	FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FTCTTGAAGGG FATTGAATGTT FATTGAATGTT FATTGAATGTT	GATCCTTACC GATCCTTACC  *  TGCCAAGCCII TGCCAAGCCII  *	TGAAGC TGAAGC TGAAGC 1200  ACACCC NCACCC	757 729 170 32 32 783 764 230

•

	* 1280	*	1300	*	1320	
LpPEPCb1					:	-
LpPEPCb2					:	-
LpPEPCb3					:	_
LpPEPCb4					:	_
LpPEPCb5	AGTTCGCTGATGAGAAGGAGC	CAGCTGAGCTG	GTGCAACTGAAC	CGTGGGAGCG	AGTACG	350
LpPEPCb6	AGTTCGCTGATGAGAAGGAGC	CAGCTGAGCTG	GTGCAACTGAAC	CGTGGGAGCG	AGTACG	212
•				CICCOCCC	ACHAGE .	2.12
	* 1340	*	1360	*	1380	
LpPEPCb1					1360	_
						-
LpPEPCb3					•	
LpPEPCb4						_
LpPEPCb5		TCATCCTTACC	ATCAACCCTA TO	PCCTCTCC A	WC C 2 2 2	400
	CCCCAGGCCTGGAGGACACCC	TCATCCTTACCA	AIGAAGGGIA <mark>E</mark> I.	IGCIGIGGAA	TIGCAAA :	409
בפינים	CCCCAGGCCIGGAGGACACCC	ICAICCI IACCA	AIGAAGGGIAII	IGCIGIGGAA	TGCAAA:	272
	* 1400	_	1400		9 4 4 5	
LpPEPCb1 :		<b></b>	1420	*	1440	
LpPEPCb1						-
LpPEPCb3						-
LpPEPCb4					:	-
LpPEPCb5	A CA CA COCONA COCONA				:	_
	ACACAGGCTAGGCCAGTTTGC	CTA-TTGGAATA	AACTGTCATECC	TCAGATGGG	GCGTGA:	
LpPEPCb6 :	ACACAGGCTAGGCCAGTTTGC	CTATTTGGAATA	AACTGTCATCCC	TCAGAT-GG	GCGTGA:	331
		·				
I - Dunck a	* 1460	*	1480	*	1500	
LpPEPCb1 :					:	-
LpPEPCb2 :						-
LpPEPCb3:					:	-
LpPEPCb4:					:	-
LpPEPCb5:		PAGTGAACCCTC	GAGGCATTTTGG	CCACTTACA	IGCCIT :	528
LpPEPCb6 :	ATATGTGTGTTCCCCAAATGC	PAGTGAACCCTC	GAGGCA-TTTGG	CCACTTACA	IGCCTT:	390
			5 775			
	* 1520	*	1540	*	1560	
						-
LpPEPCb2 :					:	-
LpPEPCb3:					:	_
LpPEPCb4:					:	_
LpPEPCb5:	TTGGTTATGNAC-TTGAT	CTTAATGNCAA	GGGTTGTTGAAG	CCTGATCTA	AATAA:	587
LpPEPCb6:	TTGGTTATGGATGNACTTTGAT	PCTTAATGÉCAA	҈Ѿ҈GGTTGTTGAAG	CCTGATCTA	AATNAA :	450
			2 21,0213 (00			
	* 1580	*	1600	*	1620	
LpPEPCb1 :					:	-
LpPEPCb2 :					:	-
LpPEPCb3 :	~				:	-
LpPEPCb4 :	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~				:	_
LpPEPCb5:	ATATGGAACAATGATATTCTG	-NGGATCTAAT	AATTTGCTTGGC	TCTGGCATCO	SNAATA:	646
LpPEPCb6 :	ATATGGAACAATGATATTCTGG	TIGITTCTTA-			:	482
			•			
	* 1640		•			
LpPEPCb1 :		-				
LpPEPCb2 :		-				
LpPEPCb3 :		-				
LpPEPCb4 :		-				
LpPEPCb5 :	GNGATTTGGAGTNGTTTAAC	666				
LpPEPCb6 :						
-						

#### ure 47 Nucleotide sequence of LpPEPCc

\* 80 \* 100 \* 120 LpPEPCc : GCACACTGAATATGGTCGGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTG : 120

\* 140 \* 160 \* 180 LpPEPCc : GAGGCATAGAATCGCTCCGTGCAATTCCATGCATCTTTGNTTGGACACAGACAAGGNTTN : 180

\* 200 \* 220

LPPEPCc : ATNTTCCTGTATGNCTTGNATTCGNCTCCACCCCCCNTA : 224

### Deduced amino acid sequence of LpPEPCc

Lppepcc : XSXLXXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIPCIFXWTQTRXX : 60

LpPEPCc : XPVXLXFXSTXTP : 73

Lppepcd	:	* 20 * 40 * 60 GTTNCTGGAACNAAGGATCTTCTTGAAGGTGATCCCTACCTGAAGCAGCGGCTCCGCCTC	:	60
Lppepcd	:	* 80 * 100 * 120 CGTGACGCGTACATCACCACCATGAACGTATGCCAGGCCTACACATŢGAAGCGGATCCGT	:	120
LpPEPCd	:	* 140 * 160 * 180 GACCCAGACTACCACGTCGCACTGCGGCCCCATCTTTCCAAGGAGGTTATGGACACAAGC	:	180
LpPEPCd	:	* 200 * 220 * 240 AAGCCGGCTTCCGAGCTTGTGACGCTGAACCCGGCCAGCGAGTACGCCCCGGGGCTGGAG	:	240
LpPEPCd	:	* 260 * 280 * 300 GACACCCTCATCTTGACCATGAAGGGCGTTGCTGCCGGTCTGCAAAACACCGGTTAGGGC	:	300
LpPEPCd	:	* 320 * 340 * 360 CAGGAGAGATGCCTGATCACCATCTTTTTGTATCTTCATGATGATGCGATGTTTTTCTTT	:	360
LpPEPCd	:	* 380 * 400 * 420 AGTCGTTTGCGGTGGGCCTTATATCTCTCGGACGTAGCTGCATCTGTCTCCCTGCTCAGT	:	420
Lppepcd	:	* 440 * 460 * 480 GAGGAATAATGGCGTTTCGCCCAAGTATATTGATAAATAA	:	480
LpPEPCd	:	* 500 * 520 AGATTTGTTTGTTAGTAATTGTTCTATTTTTTGCGAAAAAAAA		

### are 50 Deduced amino acid sequence of LpPEPCd

\* 20 \* 40 \* 60 Lppepcd : VXGXKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTLKRIRDPDYHVALRPHLSKEVMDTS : 60

\* 80

Lppepcd : KPASELVTLNPASEYAPGLEDTLILTMKGVAAGLQNTG : 98

LpPEPCe : GTTACACGCGCAGTTTGCTTGTTAGCAAGGNAGATGGCTGCTAACTTGTACTTCTCAG : 60 LPPEPCe : ATAGAAGATCTGATGTTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT : 120 LPPEPCe : GCAGATGAAGTACATCTGTCCTCAAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG : 180 LpPEPCe: AAGCAAGTTCCTCCAAATGAACCTTATCGTGTCATACTTGGCGATGTCAGGGATAAACTG: 240 LPPEPCe : TACTATACGCGCGAACGTTCTCGCCACATATTGACAACTGGAATTTCAGACATTCCAGAA : 300 LPPEPCe : GNGTCAACTTTTACTAATGTTGAACTGTTTCTGGAACCTCTTGAGCTGTGCTACAGATCC : 360 LPPEPCE: TTATCTTNCTGTGGNGACAANCTATTGCTGANGGAAGCCTTCTTGATTTCTNGCGNNCN: 420

LpPEPCe : GNATCNACTTTGTGGGCTTACTCTNGCGAA : 450

#### ure 52 Deduced amino acid sequence of LpPEPCe

\* 20 \* 40 \* 60 LpPEPCe : VTRAVCLLARXMAANLYFSQIEDLMFELSMWRCSDELRVRADEVHLSSKKKSAKHYIEFW : 60

\* 80 \* 100 \* 120

LPPEPCe : KQVPPNEPYRVILGDVRDKLYYTRERSRHILTTGISDIPEXSTFTNVELFLEPLELCYRS : 120

\* 140 \*

LpPEPCe : LSXCXDKXIAXGSLLDFXXXXXTLWAYSXE : 150

LpPEPCf	:	* GGGGTGGTGGCCCTNCT	20 FCACCTIGCCTNC	* CTGTCTCA	40 NCCACCAGNCAC	* AATCAACG	60 GAT	:	60
Lppepcf	:	* CACTCCGGGTGACTGT	80 FCAAGGTGAAGTT	* ATTGAGCA	100 GAGCTTTGGGGA		120 TGT	:	120
LpPEPCf	:	* GCTTCAGGACGCTGCA	140 GCGTTTCACAGCT	* GCTACTCT	160 TGAGCATGGGAT	* rgcgtccac	180 CCA	:	180
LpPEPCf	:	* TTTCACCAAAGCCAGA	200 GTGGCGAGCTCTT	* 'CTTGATG	220 AGATGGCTGTGG	* TTGCAACTG	240 BAGG	:	240
LpPEPCf	:	* AATACCGGTCAATCGT	260 CTTCCAAGAACCA	* \CGCTTCGT	280 PCGAGTATTTCC	* ECCTTGCA	300 ACAC	:	300
LpPEPCf	:	* CAGAGACAGAGTATGG	320 CAGGATGAATATA	* \GGAAGCA(	340 GCCATCAAAGA	* GAAAACCAA	OBE DTD/	:.	360
LPPEPCf	:	* GTGGCATTGAATCACT	380 CCGTGCAATTCC	* ATGGATCT	400 TCGCATGGACGC	* AGACACGG'	420 FTCC	:	420
LpPEPCf	:	* ACCTTCCAGTCTGGTT	440 GGGCTTTGGTGG	* rgcattca	460 AGCAȚATCCTCA	* AGAAGGAC	480 ATCA	:	480
LpPEPCf	:	* GAAATTTCCATATGCT	500 CCAGGAGATGTA	* CAACGAGT	520 GGCCATTTTCA	* GGGTCACG.	540 ATCG	:	540
LpPEPCf	:	* ATCTTGTTGAGATGGT	560 GTTCGCCAAGGG	* TAACCCTG	580 GCATTGCTGCCT	·* TGTATGAC	600 AGGC	:	600
LpPEPCf	: :	* TCCTGGTTTCAGAGGA	620 AGCTACAGCCACT	* GGGTGACA	640 AGCTGAGG : 6	344			

#### ure 54 Deduced amino acid sequence of LpPEPCf

\* 20 \* 40 \* 60

LpPEPCf : GGGPXHLAXLSXPPXTINGSLRVTVQGEVIEQSFGEBHLCFRTLQRFTAATLEHGMRPPI : 60

\* 80 \* 100 \* 120

LpPEPCf : SPKPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSRPSKRKPSG : 120

\* 140 \* 160 \* 180

LpPEPCf : GIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNFHMLQEMYNEWPFFRVTID : 180

\* 200 \*

LpPEPCf : LVEMVFAKGNPGIAALYDRLLVSEELQPLGDKLR : 214

## Figure 55 Consensus contig nucleotide sequence of TrMDHa

		* 20 * 40	* 60		
TrMDHa	:	GGCTTCTTAAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTC	TTCGATCTATTTCCA	:	60
		•			
		* 80 * 100	* 120		100
TrMDHa	:	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGA	CAAATTGGGTATGCT	:	120
		* 140 * 160	* 180		
TrMDHa	:	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAG		. :	180
		* 200 * 220	* 240		
TrMDHa	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAA	ATGGAGTTGGTGGAT	:	240
		* 260 * 280	·* 300		
TrMDHa	:			:	300
	•			-	
		* 320 * 340	* 360		
TrMDHa	:	GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGA	\GGTATGGAGAGGAAA	:	360
		* 380 * 400	* .420		
TrMDHa	:			:	420
	•				
		* 440 * 460	* 480		
TrMDHa	:	GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAA	LACCAATGCATTGATC	:	480
			•		
		* 500 * 520	* 540		
TrMDHa	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGC		:	540
		•	•		
		* 560 * 580	* 600		
TrMDHa	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAA	AGTTTCTGATGTGAAA	:	600
		* 620 * 640	* 660		
TrMDHa	:	AATGTTATAATATGGGGGAAATNATTCATCAACTCAATACCCTG		:	660

TrMDHa : CGTTAAAATCTCCT : 674

40 20

TrmDHa : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD : 60

100

TrmDHa : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMTKNVSIYKSQASALEKH : 120

180 160 TrmDHa : AAANCKVLVVANPANTNALILKEYAPSIPEKNISALTRLDHNRALGQISERLNVEVSDVK : 180

200

TrmDHa : NVIIWGKXFINSIPXCXPXNR : 201

ure 57 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHa

		* 20 * 40 * 60		
TrMDHa1		GIWITTCTTGWAAACNCMCTAAIIWTCTTTTCTATTGTWCTWATTTCTTCGATCTATTTCCA	:	60
TrMDHa2		-GCNACNTAMAACCMCITATINTWCTNACCTCTATTGTTCTTATTTCTTCGATCTATATCCA		59
TrMDHa3	•	-GCNTCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA	•	57
TrMDHa4	•	-GCATCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA		57
TrMDHa5	:	CTTCTT-NAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC-	:	55
TrMDHa6	:	CNTEAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTT	:	54
TrMDHa7	:	GCANTAAACTCTTTTNTATTGTTCTTNTTTCTTCGATCTATTTCC-	:	45
TrMDHa8	:		:	45
TrMDHa9	:	CACT-AACTCTTTTCT-TTGTTCTTMTTTCTTCGATC-ATTTCC-	:	41
TrMDHa10	:	TAAACTCTTÄTCTATTGTTCTTÄTTTCTTCGATCTATTTCC-	:	41
TrMDHall	•	AAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA		41
	•		•	
TrMDHa1		* 80 * 100 * 120	•	
TrMDHa1	•	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCjjcTgGTGCTGCAGGACAACTTGGGTATGCT ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT	:	120
TrMDHa2	•		:	119
TrMDHa4	:	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT	:	117
TrMDHa5	:	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAGTTGGGTATGCT	:	117
TrMDHa6	:	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT	:	115 114
TrMDHa7	•	ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAGTTGGGTATGCT ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT	:	104
TrMDHa8	•	and the same of th	:	104
TrMDHa9	•	ATGGCC-AAGACCCAGTTCGTGTTCTTGT-CCTGCTGCAGGACAAATTGGGTATGCT ATGGCC-AAGACCCAGTTCGTGTTCTTGT-ACTGGTGCTGCAGGACAACTTGGGTATGCT	:	. 99
TrMDHa10	:	ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT	:	100
TrMDHa11	:	ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT	•	101
TIMBRATI	•	A TOUCHARDACCCAGIICGIGIICIIGICACIGGIGCIGCAGGACAAAIIGGGIAIGCI	•	TOT
		* 140 * 160 * 180		
TrMDHa1	:	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC	:	180
TrMDHa2	:	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCACCTCGTGTCCTCTCACCTTGTGATGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179
TrMDHa2 TrMDHa3	:	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	: : :	179 177
TrMDHa2 TrMDHa3 TrMDHa4	:	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5	: : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177 175
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6	: : : : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177 175 174
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7	: : : : : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177 175 174 164
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177 175 174 164 163
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa8	•	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	: : : : : : : : : : : : : : : : : : : :	179 177 177 175 174 164 163 159
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	:	179 177 177 175 174 164 163 159 160
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa8	: : : : : : : : : : : : : : : : : : : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	: : : : : : : : : : : : : : : : : : : :	179 177 177 175 174 164 163 159
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC	: : : : : : : : : : : : : : : : : : : :	179 177 177 175 174 164 163 159 160
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC		179 177 177 175 174 164 163 159 160 161
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11	: : : : : : : : : : : : : : : : : : : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC ATGCTTGACATTNCACCTGGAG	: : : : : : : : : : : : : : : : : : : :	179 177 177 175 174 164 163 159 160 161
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11	: : : : : : : : : : : : : : : : : : : :	CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGAGTTGATGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCAGCGTGTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa1 TrMDHa2 TrMDHa2 TrMDHa3 TrMDHa3		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGACCGGTGTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTTGATCCTCCAC CTTGTCCCTATGATTCCACCTGGAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa5 TrMDHa6		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTGGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCACCTGCAGCCGAATCACTCAACGGTGTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235 234
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa6 TrMDHa6 TrMDHa7		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCACCTGCAGCCGAATCACTCAACGGTGTAAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235 234 224
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa6 TrMDHa7 TrMDHa7 TrMDHa6 TrMDHa7 TrMDHa7		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTCACCTGGAG ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235 234 224 223
TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11  TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa5 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa7 TrMDHa8 TrMDHa9		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTGCTAGGGGAGTGATCCTCGACCGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATTGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235 234 224 223 219
TrMDHa2 TrMDHa4 TrMDHa5 TrMDHa6 TrMDHa7 TrMDHa8 TrMDHa9 TrMDHa10 TrMDHa11 TrMDHa11 TrMDHa11 TrMDHa2 TrMDHa3 TrMDHa4 TrMDHa4 TrMDHa6 TrMDHa7 TrMDHa7 TrMDHa6 TrMDHa7 TrMDHa7		CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC CTTGTCCCTATGATTCACCTGGAG ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT		179 177 177 175 174 164 163 159 160 161 202 239 237 237 235 234 224 223

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TAMBHAA : GCTGCATTCCCTTTCTTAAAGGGATTGTTGCTACAACTGATGTGTTAGGGCATGCACT : ACTMONA : GCTGCATTCCCTTCTTTAAAGGATTGTTGTTGTAACTGATGTGTTGGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTTCTTAAAGGGTTGTTGTTGTAAACTGATTGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTTCTTAAAGGGTTGTTGTTAAACTGATTGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTTCTTAAAGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTCTCTTAAAGGGATTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTCTCTTAAAAGGATTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : ACTMONA : GCTGCATTCCCTCTCTTAAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : ACTMONA : GCTGCAATAATTGCCGTTATGGTTGGTGGGGTTCCCTAGAAAAGAAGAGGTATGAGAGGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGGTTCCCTAGAAAAGAAGAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA : ACTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAGGTATGGAGAGAAA : GTMONA : GGTGCAATAATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAGGTATGGAGAGAAA : GTMONA : GGTGCAATAATTGCCGTTATGGTTGTGGTGGGTTCCCTAGAAAAAAAA	TrMDHa2	GCTGCA	TTCCCTCT	TCTTAAAGGAG	TTGTTGCTA	CCACTGATGT	GGTTGAGGCA	TGCACT :	29
TMDHA4 : GCTGCATTCCCTCTCTTAAAGGGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1 : 1	TrMDHa3	· GCTGCA	TTCCCTCT'	TCTTAAAGGAG	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TIGCACT:	29
TYMDHAS : GCTGCATTCCCTCTCTTAAAGGGGTGTTGCTACAACTGATGTGTTAGGCATCACTT : 2 TYMDHAG : GCTGCATTCCCTCTCTTAAAGGGATGTTGTGTAAACTGATGTGGTTAGGCATGCAT		- GCTGCA	TTCCCTCT'	TCTTAAAGGAG	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT:	: 29
TMDHa6 : GCTGCATTCCCTCTTTANAGGGGTTGTTGCTACATGTGGTTGAGGCATGCACT : 2 TMDHa7 : GCTGCATTCCCTCTCTTANAGGGGTTGTTGCTACAACTGATGTGGTTAGGGCATGCACT : 2 TMDHa9 : GCTGCATTCCCTCTTTANAGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa9 : GCTGCATTCCCTCTTTANAGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa11 : GCTGCATTCCCTCTTTTANAGGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa11 : GCTGCATTCCCTCTTTTANAGGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa11 : GCTGCATTCCCTCTTTTANAGGGGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa11 : GCTGCATTCCCTCTTTTANAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TMDHa21 : GCTGCATATATTGCCGTTATGGTTGGGTGGGTTCCCTAGAAAAGAAGGTTATGGAGAGGAAA : 3 TMDHa2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TMDHa2 : GCTGCAATATTGCCGTTATGGTTGGTGGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TMDHa2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TMDHA2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TMDHA2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TMDHA2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAGGGTATGGAGAGGAAA : 3 TMDHA2 : GCTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAGGGTATGGAGAGGAAA : 3 TMDHA2 : GGTGCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAA		GOTGCA	TTCCCTCT	TCTTAAAGGAG	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT :	: 29
TAMBHA : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATTGCACT : 2 TAMBHA : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTTCTTAAAGGAGTTGTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TAMBHA : GCTGCATTCCCTCTTCTTAAAGGAGTTGTGCAACACTGATGTGAGGAGAACACCAATGCATTGAGAGGAACACCAATGCATTGAGAGGAACTGCAACACCAATGCATTGAACAACTGAACACTGAACACCAATGCATTGAGAGGAACACCAATGCATTGAGAGGAACACAACACCAATGCATTGAGAGGAACACTTCAACACTGAACAACACCAATGCATTGAACAACACACAATGCATTGAGAGGAACACCAATGCATTGAGAGGAACACAACACCAATGCATTGAACAACTGAACAACACCAATGCATTGAGAGAACAACACCAATGCATTGAGAGAACACTTCAACACTGAACAACACAACACCAATGCATTGAGAGAACACTTCAACACTGAACAACACAACACCAATGCATTGAGAGAACACTTCAACACTCAACACCAACACACCAATGCATTGAACAACACTCTCAACACCCAACAACACCAATGCATTGACACAACAACACCAATGCATTTACAACACTTCAACACCCAACCAA		· GCTGCA	ТТСССТСТ	TCTTAAAGGAC	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT :	: 29
TYMDHAB : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TYMDHAD : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TYMDHAD : GCTGCATTCCCTCTCTTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TYMDHAD : GCTGCATTCCCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2 TYMDHAD : GCTGCATTCCCTCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2 TYMDHAD : GCTGCATTCCCTCTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2  TYMDHAD : GCTGCAACTTTGCCCTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 TYMDHAD : GGTGCAACTATTGCCCTTATGGTTGGTGGTTCCCTAGAAAAGAAAG		· CCTCC	TTCCCTCT	TCTTAAAGGAG	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT :	: 28
CTEMBLAS : CCTCCATTCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGATGCACT : 2 TYMBHAIL : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 2 TYMBHAIL : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGTTGAGGCATGCACT : 2  * 320 * 340 * 360  TYMBHAI :		· GCTGCA	TTCCCTCT	TCTTAAAGGAC	TTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT :	: 28
TYMDHa10: CCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT: 2  CTMCHa11: CCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT: 2  * 320 * 340 * 360  **TMDHa2: GGGGTCAATATTGCCGTTATGGTTGGGGGTTCCCTAGAAAAGAAGGTATGGAGGAAA : 3  **TMDHa3: GGTGTCAATATTGCCGTTATGGTTGGGGTTCCCTAGAAAAGAAGGTATGGAGGAAA : 3  **TMDHa4: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGGAAA : 3  **TMDHa4: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGGAAA : 3  **TMDHa5: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa6: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa7: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa8: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa9: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa2: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa3: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa3: GATGTGAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTTATGGAGAGGAAA : 3  **TMDHa4: GATGTGAAGAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  **TMDHB3: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  **TMDHB4: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  **TMDHB4: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ***TMDHB4: GATGTGATGACAAACTGCAAGGTTCTTGTTTTTCCCAACCCAGCAAACACCAATGCATTGATC : 4  ***TMDHB4: GATGTGATGAAACTGCAAGGTTCTTGTTTTTTCCCAACCCAG		· CCTCC	TTCCCTCT	TCTTD	ттсттсста	CAACTGATGT	GGTTGAGGCA	TGCACT	: 27
* 320 * 340 * 360  FYMDHa1:  ***  ***  ***  ***  ***  **  **  **		COTTO	TTCCCTCT	TCTTTN N N GGA(	a	CAACTGATGT	GGTTGAGGCA	TGCACT	: 28
* 320 * 340 * 360  ITMDHa1:  ITMDHa2: GGGGTCAATATTGCCGTTATGGTTGGGGGTTCCCTAGAAAAGAAGTATGGAGAGAA : 3  ITMDHa3: GGTGTCAATATTGCCGTTATGGTTGGTGGGGTTCCCTAGAAAAGAAGGTATGGAGAGAA : 3  ITMDHa3: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAA : 3  ITMDHa4: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAA : 3  ITMDHa5: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGTATGGAGAGAAA : 3  ITMDHa6: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCTTAGAAAAGAAGTATGGAGAGGAAA : 3  ITMDHa7: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCTTAGAAAAGAAGTATGGAGAGGAAA : 3  ITMDHa8: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGAGTATGGAGAGGAAA : 3  ITMDHa8: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGAGGTATGGAGAGGAAA : 3  ITMDHa9: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGAGTATGGAGAGGAAA : 3  ITMDHa9: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3  ITMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3  ITMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTATGGAGAGGAAA : 3  ITMDHa1: GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGTATGGAGAGGAAA : 3  ITMDHa2: GATGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAATATGGAGAGGAAA : 3  ITMDHa3: GATGTGAATAATGCCGTTATGGTTGGTGGGTTCCCCTAGAAAAACAT : 4  ITMDHa4: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa6: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa6: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa1: GATGTGATGACAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  ITMDHa2: GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  ITMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTCCCACCCA		GCTGC	TTCCCTCT	TCTTAAAGCAC	TTTGTTGCTA	CAACTGATGT	GGTTGAGGCA	TGCACT	: 28
TYMDHa1: GGGGTCAATATTGCCGTTATGGTTGGGGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA 3 GTMDHa3: GGTGTCAATATTGCCGTTATGGTTGGGGGTCCCTAGAAAAGAAGGTATGGAGAGAAA 3 GTMDHa3: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA 3 GTMDHa6: GGTGTCAATATTGCCGTTATGGTTGGTGGGTCCCTAGAAAAGAAGGTATGGAGAGAAA 3 GTMDHa6: GGTGTCAATATTGCCGTTATGGTTGGTGGTGTGCTAGAAAAGAAGGTATGGAAGGAA	TIMDNATI	: GC1GCF	ALLCCICL	ICITATACCA	311011002.		-		
TYMDHa1:  GGGGTCAATATTGCCGTTATGGTTGGGGGGTTCCCTAGAAAAGAAGGTATGGAGGGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  TYMDHa6:  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGTATGGAGAGAAA  TYMDHa6:  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCTAGAAAAGAAGTATGGAGAGAAA  TYMDHa7:  GGTGTCAATATTGCCGTTATGGTTGGTGGTTGGTTMAAAAAGAAGGTATGGAGAGAAA  TYMDHa8:  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  TYMDHa10:  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  TYMDHa11:  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAAA  TYMDHa11:  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAGGTATGGAGAGAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAGGTATGGAGAGAAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAGGTATGGAGAGAAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAGGTATGGAGAGAAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAGGTATGGAGAGAAAA  GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAAAAA			*	320	*	340	*	360	
TYMDHA2 : GGGGCAATATTGCCGTTATGGTTGGGGGTTCCCTAGAAAGAGGGTATGGAGAGAA : 3 TYMDHA3 : GGTGTCAATATTGCCGTTATTGGTTGGTGGTTCCCTAGAAAGAGAGGTATGGAGGGAA : 3 TYMDHA5 : GGTGTCAATATTGCCGTTATTGGTTGGTGGTTCCCTAGAAAGAA	m-MDU-1		<del>-</del>						:
IMMHBB3 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAGAGGTATGGAGAGGAA : 3 ITMDHB45 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAGAA		. cocom	TA ATTA TTCC	CCTTATCCTT	SCEEGETTCC	CTAGAAAAG	AGGTATGGAG	AGGAAA	: 35
TYMDHA4 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTTCCTAGAAAAGAAGGTATGGAGGAAA : 3 TYMDHA5 : GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCTAGAAAAGAAGGTATTGGAGAGGAAA : 3 TYMDHA6 : GGTGTCAATATTGCCGTTATGGTTGGTGGTTCTAGAAAGAA		COTOTO	AAIAIIGC	CCTTATCCTT	GETCCCTTCC	CTAGAAAAG	AGGTATGGAG	EAGGAAA	: 35
TYMDHAS: GGTGTCATATTGCCGTTATGGTTGGTGGTTCCTTAGAAAGAGGTATGGAGGGAAA : GTYMDHAG : GGTGTMAATATTGCGTTATGGTTGGTGGGTTCCTTAGAAAGAAGGTATGGAGGGAAA : GGTGTCAATATTGCCGTTATGGTTGGTTGGTTCCTTAGAAAGAA			TANTAITICC	CGTTATCCTT	GETEGETTE	CTAGAAAAG	AGGTATGGA	SAGGAAA	: 35
TYMDHa6: GGTGTWATATTCACCATATGGTGGGGGTTTGTAAAACAAGGTTATGAAGAAAAAAAA		COTO	TANTATIGC	CGTTATCGTT	COTCCCTTCC	CTAGAAAAG	AAGGTATGGA	SAGGAAA	: 35
TYMDHA1: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGAGAGAGA		· CCTCT		CGNTATGGNT	อยายอยาานี เหมายอยู่ชื่อย	NTAĞNANACI	AAGGTNT		: 34
ITMDHa8 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGGAAA : 3 ITMDHa9 : GGTGTCAATATTGCCGTTATGGTTGGTGGTTCCCTAGAAAAGAAGGTATGGAGAGAA : 3 ITMDHa10 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAGTATGGAGAGAA : 3 ITMDHa11 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAGAGTATGGAGAGAA : 3 ITMDHa11 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAGAGTATGGAGAGAA : 3 ITMDHa11 : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGATTGGAGAGAAA : 3 ITMDHa2 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa3 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa4 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa5 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa6 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa9 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa9 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa10 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa11 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa12 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa3 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa4 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa5 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa6 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa6 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa8 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 ITMDHa9 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGTCCCAACCCAGCAAACACCCAATGCATTGATC : 4 ITMDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTTGTCCCAACCCAAGCACCCAATGCATTGATC : 4 ITMDH		· GGIGIT	TAATATIGA TAATATTCO	CGTTATGETT	GGTGGGTTC	CTAGAAAAG	AAGGTATGGA	SAGGAAA	: 34
ITMDHa9: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 ITMDHa10: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 ITMDHa11: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAÑAAAAGAAGGTATGGAGAGGAAA : 3 ITMDHa11: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAÑAAAAGAAÑGTATGGAGAGGAAA : 3 ITMDHa2: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa3: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa5: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 ITMDHa6:		COTOTO		CGTTATGGTT	GGTGGGTTC	CTAGAAAAG	AAGGTATGGA	GAGGAAA	: 34
ITMDHa10: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 3 ITMDHa11: GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAÑAAAAGAAGATGTATGGAGAGGAAA : 3  * 380 * 400 * 420  ITMDHa1: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa2: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa5: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4  ITMDHa6:		· COTOTO	CAMIATIGE	TEDDIATION	ССТЕВВВТОВ	CTAGAAAAG	AAGGTATGGA	GAGGAAA	: 33
* 380 * 400 * 420  ITMDHa1: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa2: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa5: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa6: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa6: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa7: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa9: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAAGCCTTTGACCCATTGACC  * 440 * 460 * 480  ** 440 * 460 * 480  ** TMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa6: TTMDHa6: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa8: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC ITMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC		GGTGTC	CAATAIIGC	CGTTATCGTT CGTTATCGTT	GGTGGGTTC(	CTAGAAAAG	AAGGTATGGA	GAGGAAA	: 34
* 380 * 400 * 420  ITMDHa1:  ITMDHa2: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa3: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa6:  ITMDHa7: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa8: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa9: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAGGCCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAGGCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAGGCTTCTGCCCTTGAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAGGCTTTGTCCCCTTGAAAAAACAT  ITMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAAGCCTTTGACCAACAAAAAAACAT  ITMDHa11: GATGTGATGAAAAAATGTCTCTATTTACAAGTCTTAAGCCTTTGACCAACCCAAGCAAACACCAATGCATTGATC  ITMDHa11: GATGTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAAGCACCCAATGCATTGATC  ITMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAAGCACCCAATGCATTGATC		CCTCTC	CAAIAIIGC	CGTTATCGTT	GGTGGGTTC	CTANAAAAG	AANGTATGGA	GAGGAAA	: 34
TYMDHA1:  GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA3:  GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA4:  GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA5:  GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA6:  TYMDHA6:  GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA7:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA8:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA9:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA10:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11:  GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11:  GATGTGATGACAAAAAAAATGTCTCTATTTACAAGTCTTAAGGCTTTTGTGTCCCCTTGAAAAACACTAAAAAAACAT  TYMDHA2:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA4:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA6:  TYMDHA7:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA8:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA8:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAACACCCAATGCATTGATC  TYMDHA9:  GCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAACACCCAATGCATTGATC			,					•	
TYMDHa2: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa3: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa5: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa6: TYMDHa7: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa8: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa9: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 IYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAAGGCTTTTTGTCCCTTTGAAAAAACAT : 4 IYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTTAAGGCTTTTTTGTCCCAACCCAGCAAACACCAATGCATTGATC : 4 IYMDHa2: GCTGCTGCAAACTGCAAGGTTCTTTTTTTTTTTTTGCAACCCAGCAAACACCAATGCATTGATC : 4 IYMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 IYMDHa6: TYMDHa6: GCTGCTGCAAACTGCAAGGTTCTTTGTTTTTTTTTTTTT			*	380	. *	400	*	420	•
TYMDHA2 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA4 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT  TYMDHA5 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA6 :  TYMDHA6 :  TYMDHA7 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA8 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA9 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA10 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TYMDHA11 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  * 440	TrMDHa1	:					emaccommon	AAACAT	4
TYMDHa4: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa5: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa6:  TYMDHa7: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa8: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa9: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 4 TYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTGAGCCTTGTGCCCTTGAAAAACAT : 4 TYMDHa11: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTGAGCTTTTTGTCCCTTGAAAAACAT : 4 TYMDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa4: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa5: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa6:  TYMDHa7: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa8: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAAACTGCAAGGTTCTTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAAACTGCAAGGTTCTTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAAACTGCAAGGTTCTTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAACTGCAAGGTTCTTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TYMDHa10: GCTGCTGCAACTGCAAGGTTCTTTGTTGTTGTTGCCAACCCAGCAACAC	TrMDHa2	GATGT	GATGACAAA	AAATGTCTCT	ATTTACAAG'	rcrcaggciii	CTGCCCTTGA	AMAACAI	
TYMDHA5 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA6 : TYMDHA7 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA8 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA9 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA10 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA11 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHA11 : GATGTGATGAC - AAAAATGTCTCTATTTACAAGTCTTAAAGCTTTATGACCTTTGAAAAACAT : ATMDHA1 : AAAAATGTCTCTATTTACAAGTCTTAAAGCTTTAAAAAACAT : ATMDHA1 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA4 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA5 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA6 : AAAAATGTCTTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA6 : AAAAATGTCTTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA6 : AAAAATGTCTTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA6 : AAAAATGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : ATMDHA6 : AAAAATGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTTGTTGTTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAAGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAAGGTTCTTGTTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAAGTCTTGTTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : AAAAATGTCTAAGTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : AAAAATGTCTAAGTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : AAAAATGTCTAAGTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAATGTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAATGTTGTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAAATGTCTAATGTTGTTGTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : AAAAATGTCTAATGTTGTTGTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : AAAATGTCTAATGTTTGTTGTTGTTGTTGTTGTTGTT	TrMDHa3	: GATGT	GATGACAAA	AAATGTCTCT	ATTTACAAG	rcreaggerr	CTGCCCTTGA	AAAACAI	: 4
TYMDHa6: TYMDHa7: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT TYMDHa8: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT TYMDHa9: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT TYMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT TYMDHa11: GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT TYMDHa11: GATGTGATGAC AAAAATGTCTCTATTTACAAGTCTTAAGCTTTTTGTCCCTTGAAAAACAT TYMDHa1: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC TYMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC TYMDHa4: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC TYMDHa5: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC TYMDHa6:	TrMDHa4	: GATGT	GATGACAAA	AAATGTCTCT	ATTTACAAG	TCTCAGGCTT	CTGCCCTTGA	AAAACAI	: 4
TrmDHa7 : GATGTGATGACAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : ATMDHa8 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT : ATMDHa9 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT : ATMDHa10 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAAACAT : ATMDHa11 : GATGTGATGAC—AAAAATGTCTCTATTTACAAGTCTTAAAGTCTTAAAAAACAT : ATMDHa11 : GATGTGATGAC—AAAAATGTCTCTATTTACAAGTCTTAAAGTCTTAAAAAAAA	TrMDHa5	: GATGT	GATGACAAA	AAATGTCTCT	'ATTT'ACAAG'	rcrcaggerr	CIGCCCIIGA	AAAACAI	. 4
TrmDHa8 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TrmDHa9 : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TrmDHa10 : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  TrmDHa11 : GATGTGATGAC AAAAATGTCTCTATTTACAAGTCTTAAAGCTTTTTTGAAAAACAT  * 440	TrMDHa6	:					orgoggerea.	TADAAGA	: 4
TrmDha9: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT TrmDha10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT TrmDha11: GATGTGATGAC AAAAATGTCTCTATTTACAAGTCTTAAAGCTTTTAAAGCAT  * 440	TrMDHa7	: GATGT	GATGACAAA	AAAATGTCTCT	ATTTACAAG	TCTCAGGCTT	CTGCCCTTGA	AAAACAI	: 4
TrMDHa10: GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT  * 440 * 460 * 480  TrMDHa1: GCTGCTGCAAACTGCAAGGTTCTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa2: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  TrMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  TrMDHa4: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC  TrMDHa5: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa6: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa7: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa8: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa9: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa10: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC	TrMDHa8	: GATGT	GATGACAAA	AAAATGTCTCT	ATTTACAAG	TCTCAGGCTT	CIGCCCIIGA	AAAACAI	: 4
* 440 * 460 * 480  TrMDHa1: GCTGCTGCAAACTGCAAGGTTCTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC  * TrMDHa2: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa3: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa4: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa5: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC  TrMDHa6:	TrMDHa9	: GATGT	GATGACAAA	AAAATGTCTCT	ATTTACAAG	TCTCAGGCTT	CTGCCCTTGA	AAAACAT	: 4
* 440 * 460 * 480  TrMDHa1:	TrMDHa10	: GATGT	GATGACAA	AAAATGTCTCT	'AT'I'TACAAG	TCTCAGGCTT	Encircerre	AAAACAT	: 4
TrmDHa1:	TrMDHa11	: GATGT	GATGAC-AA	AAAATGTCTCT	'ATTTACAAG	rctipaxGctt	I,TGNCCI IGA	AAAACAI	. 4
TrmDHa1:									
TrmDHa2 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAACGCTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAACGCTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCAAACTGCAAACGCTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTTGCCAACCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACACCCAATGCATTGTTGTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTCTGCAAGGTTCTTTGTTTGTTTGCCAACCCAAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACTGCAAGGTTCTTGTTTGTTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : CTGCTGCTGCAAACACCCAAGCAATGCATTGTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT			*	440	*	460	*	480	
TrmDha3 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha4 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha5 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha7 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha8 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha9 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4  TrmDha10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4	TrMDHa1	:					7070077766	ATTCATC	: 4
TrmDha4 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : CTmDha5 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTCCAACCCAGCAAACACCAATGCATTGATC : CTmDha6 :	TrMDHa2	: GCTGC	TGCAAACTO	GCAAGGTTCTT	GITIGITIGCC	AACCCAGCAA	ACACCAAIGC	ATIGATO	: 4
TrmDHa5 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : TrmDHa6 :	TrMDHa3	: GCTGC	TGCAAACT	ccaaccttctt	GAMAGAMAGGG	AACCCAGCAA	ACACCAATGC	ATTGATC	
TrmDha6 :	TrMDHa4	: GCTGC	TGCAAACT	gcaaggttct1	GIMEIMGCC	AACCCAGCAA	ACACCAAIGC	ATTGATC	
TYMDHA6 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : GCTGCTGCAAACTGCAAACTTGTTGTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAGGTTCTTGTTGTTGTTGTTGCCAACCCCAGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACACCCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAACTGCAAACACCCAATGCAATGCATTGATC : GCTGCTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACACCCAAACACCCAAACACCCAAACACCCAAACACCCAAACAC	TrMDHa5	: GCTGC	TGCAAACT	GCAAGGTTCTT	GHARGUATECE	AACCCAGCAA	ACACCAAIGC	ALLGAIC	
TrMDHa8 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TrMDHa9 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4 TrMDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 4	TrMDHa6	:					7070077000	ATTCATC	: 4
TrmDHa9 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : TrmDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : '	TrMDHa7	: GCTGC	TGCAAACT	GCAAGGTTCTT	GTTGTTGCC	AACCCAGCAA	ACACCAATGC	ATTGATC	
TrMDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC :	TrMDHa8	: GCTGC	TGCAAACT	GCAAGGTTCTI	reamieanice e	AACCCAGCAA	ACACCAATGC	ATTGATC	
TrmDHa10 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : TrmDHa11 : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGTTGTCAACCCAATGCATTGATC :	TrMDHa9	: GCTGC	TGCAAACT	GCAAGGTTCT'!	Kennkennkele	AACCCAGCAA	ACACCAATGC	ATTGATC	
TrmDHa11: GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGTTGTTGTTGTCAACACCAATGCATTGATC	TrMDHa10	: GCTGC	TGCAAACT	GCAAGGTTCT'	rennieunieee	AACCCAGCAA	ACACCAAIGC	ATTCATC	
	TrMDHa11	: GCTGC	TGCAAACT	GCAAGGTTCT	I.G.I.I.G.I.I.GIVIC	AACCCAÇCAA	ACACCAAIGC	ALICALC	. 4

TrMDHa1		* 500 * 520 * 540		
	:		: -	
TrMDHa2	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 539	
TrMDHa3	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 537	
TrMDHa4	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 537	
TrMDHa5	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 535	
TrMDHa6	:		: -	
TrMDHa7	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 524	
TrMDHa8	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 523	
TrMDHa9	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC	: 519	
TrMDHa10	:	TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTCGAC	: 520	
TrMDHa11	:	TTGAAGGAATATGCTCCATÑCATTCCTGAÑAAAAACATTTÑTGCTTTGACTAGATTGGAC	: 520	
			. 320	
TrMDHa1		* 560 * 580 * 600		
TrMDHa2	•	CATALCACCCCACITICACTO	: -	
TrMDHa3	:	CATAACAGGGCACTIGGTCA	: 559	
TrMDHa3	:	CATAACAGGGCACTAGGTCAAATTTCTGAA	: 567	
TrMDHa4	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAA	: 575	
	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	: 595	
TrMDHa6	:		: -	
TrMDHa7	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGAC	: 558	
TrMDHa8	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	: 583	
TrMDHa9	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGG	: 577	
TrMDHa10	:	CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA	: 580	
TrMDHa11	:	CATAACAGGGCACTAGGĞCAAATTTÑTGAAAÑACTAAACGTTGAAGTTTÑTGATGTGAAA	: 580	
TrMDHa1	:	* 620 * . 640 * 660	: -	
TrMDHa2	:		: -	
TrMDHa3	:		: -	
TrMDHa4	:		: -	
TrMDHa5	:	AATGTTAT-A-AT	: 606	
TrMDHa6	:		: -	
TrMDHa7	:		: -	
TrMDHa8	:	AATGTTATAAT@TGGG	: 599	
TrMDHa9	:		: -	
TrMDHa10	:	AATGTTATAATGTG	: 594	
TrMDHa11	:	AATGTTAT-ATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC	: 639	
		*	•	
TrMDHa1	:			
TrMDHa2	:			
TrMDHa3	:			
TrMDHa4	:			
TrMDHa5	:			
TrMDHa6	:	*		
TrMDHa7	:	*		
TrMDHa8				
TrMDHa9	•			
TrMDHa10	•			
TrMDHa11	0	CGTTAAAATCTCCT : 653		
TIMUGII	:	CGTTAAAATCTCCT : 653		

•

TrMDHb	:	* 20 * 40 * 60 TTCTCCCANAATCNNGAAANCGCCCANACATCACACAACATAACACCTTACTCTTC	:	60
TrMDHb	:	* 80 * 100 * 120 TCTCTNAACAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCGATTCCTTCC	:	120
TrMDHb	:	* 140 * 160 * 180 TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT	:	180
TrMDHb	: •	* 200 * 220 * 240 TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC	:	240
TrMDHb	:	* 260 * 280 * 300 CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG	:	300
TrMDHb	:	* 320 * 340 * 360 GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA	:	360
TrMDHb	:	* 380 * 400 * 420 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG	:	420
TrMDHb	:	* 440 * 460 * 480 AGGAAGGATGTGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA	:	480
TrMDHb	:	* 500 * 520 * 540 AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA	:	540
TrMDHb	:	* 560 * 580 * 600 TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTĢACTAGA	:	600
TrMDHb	:	* 620 * 640 * 660 CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT	:	660
TrMDHb	:	* 680 * 700 * 720 GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT	:	720
TrMDHb	:	* 740 * 760 * 780 GCAACTGTTAACACCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC	:	780
TrMDHb	:	* 800 * 820 * 840 TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT	:	840
TrMDHb	:	* 860 * 880 * 900 AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG	:	900
TrMDHb	:	* 920 * 940 * 960 GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC	:	960

\* 980 \* 1000 \* 1020

TYMDHb : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 1020

\* 1040 \* 1060 \* 1080

TYMDHb : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

\* · 1100

TrMDHb : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 1111

\* 20 \* 40 \* 60

TrMDHb : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD : 60

TrMDHb : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEKH : 120

\* 140 \* 160 \* 180

TrMDHb : AAANCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLNVQVSDVK : 180

\* 200 \* 220 \* 240

TrMDHb : NVIIWGNHSSTQYPDVNHATVNTPAGEKPVRELVSDDAWLNGEFISTVQQRGAAIIKARK : 240

\* 260 \* 280 \* 300

TrMDHb : LSSALSAASAACDHIRDWVLGTPQGTFVSMGVYSDGSYNVPAGLIYSFPVTTANGEWKIV : 300

TrMDHb : QGLSIDEFSRKKLDLTAEELSEEKSLAY : 328

are 60 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHb

		* 20 * 40 * 60		
TrMDHb1				47
TrMDHb2	:	TTCTCCCMAATCNNGAAANC-MCGC-ACA-CA-ACA-C-TAA-ACTACT-M-C-T-C TTCTCMCANAATCNNGAAANC-CCGC-A-A-A-ACA-C-TAA-ACTACT-M-C-T-C		45
TrMDHb3	:	GNNACCACA CALACA - CA	:	37
TrMDHb4	:			32
TrMDHb5	:	GCNCANACATAACACAACACTAAACCT NA CT - NGTC		35
TrMDHb6	:		:	27
TrMDHb7	•	TTÿ-ACĞ-TA-ACĞ-C-TAĞ-ACTCĞACT-N-C-TTC		28
TrMDHb8	•	G-NA-CCACC-TAAC-CCTGACTNN-C-TNC	:	25
TrMDHb9	•	GÑ-Ā-ÑĒC-TCACT-À-C-TŅC	:	16
TrMDHb10	:	CANCACTAMACC - JA-CT-CNCAC	:	21
TrMDHb11	•		:	21
TrMDHb12	:	AACACTAAACCC-RA-CTNCTCTC	:	22
TrMDHb13	:	CN-TAAC-CCTNACTCN-C-T-C	:	18
TrMDHb14	:		:	14
TrMDHb15	:		:	20
TrMDHb16	:	GŅĀĞÇACŅTĀĀĀĢCTNC-TŅC	:	20
TrMDHb17	:	AGCACNTAACCTT-CCTNC	:	18
TrMDHb18	:	A-CACÑT AÁCCTNC-TŅC	:	16
TrMDHb19	:	TANCET CART	:	12
TrMDHb20	:		:	7
TrMDHb21	:	rcăc	:	4
TrMDHb22	:	TC	:	2
TrMDHb23	:		:	-
TrMDHb24	:		:	-
TrMDHb25	:		:	-
TrMDHb26	:		:	-
TrMDHb27	:		:	-
TrMDHb28	:			-
TrMDHb29	:		:	-
TrMDHb30	:		:	-
TrMDHb31	:		:	-
TrMDHb32	:		:	-

	والمستشيرة				100	-	120		
:	TCT							:	104
:								:	102
:		AACAAAAA	CTGTTCTTCC	CTCTTAATC	TTCCCTGTTCG	ATTCCTTCLA	TTTCT	:	94
:	TCT : NA	AACAAAÑO	CTATTCTTCAT	CTCTTAATC	TTCGCGGTTCG	ATTCCTTCC	TTTCT	:	91
:	TCT-N-							:	91
:	TCT	Principal Section 1			E # 12	1	of the change of	:	84
:								:	85
:								:	84
:								:	72
:	TCTCA-	AAC-AAAA	стейтсттсст	CTCTTAA-C	TTCCCTGTTC	SATTCCTTCCA	GTTCT	:	78
:	TCTCTN	IAAC <mark>-</mark> AAAA	CTGTTCTTCCT	CTCTTAATC	TTCCCTGTT[]	SATTCCTTCCA	GTTCT	:	80
:								:	81
:								:	<b>7</b> 5
:								:	71
:								:	79
:								:	78
:								:	76
:								:	74
:	TCT-NA							:	70
:	TWA							:	63
:								:	63
:	TCT N							:	59
:								:	51
:		AAAA						:	49
:								:	46
:			- ggttcttc-c	CTCTTATIC	TTCCCTGTTC	ATTCCTTCT	ATTTCT	:	44
:			TTCCI	CTCTTNATC	TTCCCTGTTI	SATTCCTTCC-	GTTCT	:	39
:								:	-
:								:	-
:								:	-
:								:	
<b>:</b> .								:	-
		TOT - NA TOT	TCT - AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TCT - AAACAAAACTGTTCTTCCT TTA - AACAAAAACTGTTCTTCCT TTA - AACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCTT TTM - AACAAAAACTGTTCTTCTT TCT - NAACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCCT TCTCT - AACAAAAACTGTTCTTCCT TCTCT - NAACAAAAACTGTTCTTCCT TCTCT - NAACAAAAACTGTTCTTCCT TCTCT - AAAAAAAACTGTTCTTCCT TCTCT - AAAAAAAACTGTTCTTCCT TCTCT - AAAAAAAACTGTTCTTCCT TCTCTAAC - AAAAACTGTTCTTCCT TCTCTAACAAAAAACTGTTCTTCCT TCTCTAACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCCT TCT - NAACAAAAACTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	TOT - AAACAAAACTGTTCTTCCTCTTTAATC  TNA - AACAAAAACTGTTCTTCACTCTTAATC  TOT NAACAAANGCTATTCTTCACTCTTAATC  TOT NAACAAANGCTATTCTTCATCTCTTAATC  TOT NAACAAAACTATTCTTATCTTTAATC  TOT NAACAAAACTATTCTTAATCTTAATC  TOT NAACAAAACTATTCTTAATCTTAATC  TOT NAACAAAACTATTCTTAATCTTTAATC  TOT NAACAAAAACTATTCTTCATCTTTAATC  TOT NAACAAAAACTGTTCTTCTCTTTAATC  TOT NAACAAAACTGTTCTTCTTCTTTAATC  TOT NAACAAAACTGTTCTTCTTCTTTAATC  TOT NAACAAAACTGTTCTTCTTCTTTAATC  TOT NAACAAAAACTGTTCTTCTTCTTTAATC  TOT NAACAAAAACTGTTCTTCTTCTTTAATC  TOT AAAAAAACTGTTCTTCTTCTTTAATC  TOT CAAACAAAAACTGTTCTTCTCTTTAATC  TOT CAAACAAAAACTGTTCTTCTCTTTAATC  TOT CAAACAAAAACTGTTCTTCTCTTTAATC  TOT NAACAAAAACTGTTCTTCTCTTTAATC  TOT NAACAAAAACTGTTCTTCTCTCTTTAATC  TOT NAACAAAAACTGTTCTTCTCTCTTTTATC  CAAAAACTGTTCTTCCTCTTTTATC  AAAAACTGTTCTTCCTCTTTTATC  TOT NAACAAAAACTGTTCTTCTCTCTTTTATC  TOT NAACAAAAACTGTTCTTCTCTCTTTTATC  TOT NAACAAAAACTGTTCTTCTCTCTTTTATC  TOT NAACAAAAACTGTTCTTCCTCTTTTATC  TOT NAACAAAAACTGTTCTTCTCTCTTTTATC  TOT NAACAAAAACTGTTCTTCCTCTCTTTTATC  TOT NAACAAAAACTGTTCTTCCTCTCTTTATCCTCTTTTATCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTATTCCTCTCTTTTTT	TCT AAAGAAACTGTTCTTCCTCTTAATCTTCCCTGTTIG  TTT AAAGAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTIG  TTT AACAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCT AAA AAACTGTTCTTCCTCTTTAATCTTCCCTGTTIG  TCT AAA AAAACTTTTCTTCTTCTTTAATCTTCCCTGTTIG  TCT AAAAAAACTTTTCTTCATCTTAATCTTCCCTGTTIG  TCT AAAAAAACTTTTCTTCATCTTAATCTTCCCGGGTTCC  TCT AAAAAAACTTTTCTTCATCTTAATCTTCCCGGGTTCC  TCT AAAAAAACTTTTCTTCATCTTAATCTTCCCGGGTTCC  TCT AAAAAAACTGTTCTTCATCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCT AAAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTAAC AAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTGAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTGAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTGAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTGAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTGAAC AAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTAACAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  TCTCTAACAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  CCTCTAAACAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTCC  CCAAAAACTGTTCTTCCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTAATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTAATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTATCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTTTCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTTTTCTTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTTTTCTCCCTGTTCC  CAAAAACTGTTCTTCCTCTCTTTTTTTTTCTCCTTTTTCCCTTTTCCCTTTT	TCT - AAAGAAAACTGTTCTTCCTCTTTAATCTTCCTGTTJGATTCCTTCAAACAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTJGATTCCTTCAAACAAAAACTGTTCTTCCTCTTTAATCTTCCCTGTTGATTCCTTCTTCTTCTTTAATCTTCCCTGTTGATTCCTTCC	TCT - AAAGAAACTGTTCTTCCTCTTTAATCTTCCTGTTTGATTCCTTCC	TCT AAAGAAAACTGTTCTTCCTCTTTAATCTTCCTGTTTGATTCTTCAGTTCT  TCT AAAGAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCTTCAGTTCT  TTA AACAAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCTTTTCT  TCT NAA-NAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCC

			140	*	160	*	180		
TrMDHb1	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTGT	TCTCGTC.	ACTGGTGCTGC/	AGGGCAAA'	TTGGT	:	164
TrMDHb2	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTGT	TCTCGTC	ACTGGTGCTGC	AGGGCAAA'	TTGGT	:	162
TrMDHb3	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTGT	TCTCGTC	ACTGGTGCTGC?	AGGCCAAA'	TTGGT	:	154
TrMDHb4	:	TCAGCAATGGCCAAAGA	CCCAGTTCGTGT	CCTCGTI	ACTGGTGCTGC?	AGGCCAAA'	TTGGT	:	151
TrMDHb5	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTGT	TCTCGTC	ACTGGTGCTGC?	AGGGCAAA'	TTGGT	:	151
TrMDHb6	:	TCAGCAATGGCCAAAGA	CCCAGTTCGTGT	CCTCGTI	ACTGGTGCTGC	AGGCCAAA'	TTGGT	:	144
TrMDHb7	:	TCAGCAATGGCCAAAGA	CCCAGTTCGTGT	CCTCGTI	ACTGGTGCTGC	AGGÇCAAA'	TTGGT	:	145
TrMDHb8	:	TCAGCAATGGCCAAAGA	CCCAGTTCGTGT	CCTCGT	ACTGGTGCTGC	AGG¦ÇCAAA'	TTGGT	:	144
TrMDHb9	:	TCAAAAATGGCCAAAGA	.CCCAGTTCGTGT	TCTCGTC	ACTGGTGCTGC	AGGCCAAA'	TTGGT	:	132
TrMDHb10	:	TCAAAAATGGCCNAAGA	CCCAGTTCGTGT	TCTCGTC	ACTGGTGCTGC	ŊĠĠĠĊŖŖŖ	TTGGT	:	138
TrMDHb11	:	TCAAAAATGGCCAAAGA	.CCCAGTTCGTGT	PTCTCGTC	ACTGGTGCTGC	AGGGCAAA'	TTGGT	:	140
TrMDHb12	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG	PTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	:	141
TrMDHb13	:	TCAGCAATGGCCAAAGA	CCCAGTTCGT	rectceti	ACTGGTGCTGC.	AGGCCAAA'	TTGGT	:	135
TrMDHb14	:	TCAAAAATGGCCAAAÑA	CCCAGTTCGTG	TTCTCGTC	ACTGGTGCTGC	AGGCCAAA'	TTGGT	:	131
TrMDHb15	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	:	139
TrMDHb16	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG	FTCTCGTC	ACTGGTGCTGC.	AGGĞCAAA	TTGGT	:	138
TrMDHb17	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG	TTCTCGTC	ACTGGTGCTGC	AGG <u>C</u> CAAA	TTGGT	:	136
TrMDHb18	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG	TTCTCGTC	ACTGGTGCTGC.	AGGGCAAA	TTGGT	:	134
TrMDHb19	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGÇCAAA	TTGGT	:	130
TrMDHb20	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGCCAAA	TTGGT	:	123
TrMDHb21	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	:	123
TrMDHb22	:	TCAAAAATGGCCAAAGA	CCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGCCAAA	TTEGT	:	119
TrMDHb23	:	T-NAAAATGGCCAAAGA	ACCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TIGGI	:	1.10
TrMDHb24	:	TCAAAAATGGCCAAAGA	ACCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	:	109 106
TrMDHb25	:	TCAAAAATGGCCAAAGA	ACCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	•	108
TrMDHb26	:	T-NAAAATGGCCAAAGA	ACCCAGTTCGTG'	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TTGGT	:	97
TrMDHb27	:	TC-AAAATGGCC-AAGA	ACCCAGTTCGTG	TTCTCGTC	ACTGGTGCTGC	AGGGCAAA	TIGGI	:	91
TrMDHb28	:							•	_
TrMDHb29	:							:	
TrMDHb30	:							•	-
TrMDHb31	:								_
TrMDHb32	:							•	_

TYMDHD1 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 222 TYMDHD3 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 221 TYMDHD4 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211 TYMDHD5 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211 TYMDHD6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211 TYMDHD6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TYMDHD6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TYMDHD9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TYMDHD9 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TYMDHD1 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192 TYMDHD11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TYMDHD12 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TYMDHD13 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TYMDHD13 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD14 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD15 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD16 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD17 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD18 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD19 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD20 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD21 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD22 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHD23 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHD24 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170 TYMDHD25 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHD26 : TATGCACTTGCCCTATGATTGCTAGGGGAGTGA				*	200	*	220	*	240		
TYMDHb3 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.11 TYMDHb4 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.11 TYMDHb5 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.11 TYMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.04 TYMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.05 TYMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.05 TYMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.05 TYMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.92 TYMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.92 TYMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.00 TYMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.01 TYMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   2.01 TYMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.95 TYMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.95 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.99 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.96 TYMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.83 TYMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.83 TYMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.66 TYMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.66 TYMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   1.66	TrMDHb1	:	TATGCAC	TTGTCCC	TATGATTGCT	AGGGGAGTGAT	CCTTGGTCCTC	GATCAACCTO	STGATC	:	224
TYMDHbb4 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   211 TYMDHb5 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC   211 TYMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   204 TYMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   205 TYMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   205 TYMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   205 TYMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   192 TYMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   200 TYMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   201 TYMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   201 TYMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   195 TYMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   195 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   199 TYMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   198 TYMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   196 TYMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   196 TYMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   196 TYMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   190 TYMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   190 TYMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   190 TYMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   190 TYMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   163 TYMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   170 TYMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   163 TYMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   163 TYMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC   163 TYMDHb27 : TATGCACTTGT	TrMDHb2	:	TATGCAC	TTGTCCC	TATGATTGCT	AGGGGAGTGAT	CCTTCCTC	GATCAACCTO	STGATC	:	222
TYMDHb5 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211 TYMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204 TYMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TYMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TYMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192 TYMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TYMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TYMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200 TYMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TYMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TYMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TYMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TYMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TYMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TYMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TYMDHb28 : TATGCACTTGTC	TrMDHb3	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CCTTGGTCCTC	GATCAACCTO	STGATC	:	214
TrMDHb6 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204 TrMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TrMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204 TrMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200 TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 165 TrMDHb28 : TATGCACTTGT	TrMDHb4	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	211
TrMDHb7 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205 TrMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204 TrMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192 TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200 TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 165 TrMDHb28 : TATGCACTTG	TrMDHb5	:	TATGCAC	TTGTCCC	TATGATTGCT	AGGGGAGTGAT	CCTTGGTCCTC	GATCAACCTO	STGATC	:	211
TTMDHb8 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192 TTMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TTMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TTMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TTMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TTMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TTMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191 TTMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TTMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TTMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TTMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TTMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TTMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TTMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TTMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TTMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TTMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TTMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TTMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TTMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TTMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TTMDHb28 : TATGCACT	TrMDHb6	:	TATGCAC	TTGTCCC	TATGATTGCT	AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	204
TrMDHb9 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200 TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 170 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC :	TrMDHb7	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	205
TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200 TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201 TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 170 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC : 169 TrMDH	TrMDHb8	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CGCTTGGTCCTC	GATCAACCTO	STGATC	:	204
TrmDHb11: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 201 TrmDhb13: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 295 TrmDhb14: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 195 TrmDhb15: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 191 TrmDhb16: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 199 TrmDhb16: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 199 TrmDhb18: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 196 TrmDhb19: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 194 TrmDhb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 190 TrmDhb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 190 TrmDhb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrmDhb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrmDhb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrmDhb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrmDhb26: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrmDhb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 167 TrmDhb28: TATGCACTTGCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGT	TrMDHb9	:	TATGCAC	TTGTCCC	TATGATTGCT	AGGGGAGTGAT	CGCTTGGTCCTC	GATCAACCTO	GTGATC	:	192
TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195 TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 :	TrMDHb10	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	198
TrMDHb13: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 195 TrMDHb14: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 199 TrMDHb15: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 199 TrMDHb16: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 198 TrMDHb17: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 196 TrMDHb18: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 194 TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 190 TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 170 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb26: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb29: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb29: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb29: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 165 TrMDHb28: TATGCACTGTGTCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTG	TrMDHb11	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGA'I	CCTTGGTCCTC	GATCAACCT	STGATC	:	200
TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191 TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb29 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163	TrMDHb12	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CGCTTGGTCCTC	GATCAACCT	STGATC	:	201
TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 :	TrMDHb13	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CCTTGGTCCT	GATCAACCTO	STGATC	:	195
TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198 TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196 TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194 TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190 TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183 TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179 TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb28 :	TrMDHb14	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CCTTGGTCCTC	GATCAACCTO	STGATC	:	191
TrMDHb17: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb18: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb19: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb26: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TATGCACTTGTCCTATGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC TATGCACTTGTCCTATGTCAACACTGTATAACCTGTATCAACCTGTGATC	TrMDHb15	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGA'I	CCTTGGTCCT	GATCAACCTO	STGATC	:	199
TrMDHb18: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 194 TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATÄCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:	TrMDHb16	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	198
TrMDHb19: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 190 TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATÄCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:	TrMDHb17	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	CGCTTGGTCCTC	GATCAACCTO	STGATC	:	196
TrMDHb20: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:	TrMDHb18	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGA'I	CCTTGGTCCTC	GATCAACCTO	GTGATC	:	194
TrMDHb21: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 183 TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb23: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 170 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:	TrMDHb19	:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	STGATC	:	190
TrMDHb22: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 179 TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 34 TrMDHb29: TRMDHb31: TATGCACTGTGATC: 157		:	TATGCAC	TTGTCCC'	TATGATTGCT	'AGGGGAGTGA'	GCTTGGTCCT	GATCAACCTO	STGATC	:	
TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170 TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169 TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166 TrMDHb26 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163 TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157 TrMDHb28 :		:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	GTGATC	:	
TrMDHb24: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 169 TrMDHb25: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 166 TrMDHb26: TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:		:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGA'I	GCTTGGTCCT	GATCAACCTO	GTGATC	:	
TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166  TrMDHb26 : TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163  TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157  TrMDHb28 :		:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGAT	GCTTGGTCCT	GATCAACCTO	GTGATC	:	
TrMDHb26: TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 163 TrMDHb27: TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC: 157 TrMDHb28:		:	TATGCAC	TTGTCCC	TATGATTGCT	'AGGGGAGTGA'I	GCTTGGTCCT	GATCAACCTO	GTGATC	:	
TrMDHb28 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157  TrMDHb28 : GGGGAGTGATGCTTGGTCCTGAT-NACCTGTGATC : 34  TrMDHb29 : TrMDHb30 : TrMDHb31 :		:								:	
TrMDHb28 :		:								:	
TrMDHb29 : : - TrMDHb30 : : - TrMDHb31 : : -		:	TATGCAC	TTGTCCC	TATGATTGCT					:	
TrMDHb30 : : - TrMDHb31 : : -		:				-GGGGAGTGAT	GCTTGGTCCT	GAT-NACCTO	STGATC	:	34
TrMDHb31 : : -		:								•	-
iiimmpi		:								:	-
TrmDHb32 : : -		:								:	-
	TrMDHb32	:								:	

		*	260	*	280	*	300
TrMDHb1	:	CTACACATGCTTGA	TATTCCACCC	CAGCAGAGTC	ATTGAATGG <i>I</i>	AGTTAAGATGG	AGATG
TrMDHb2	:	CTACACATGCTTGA	TATTCCÁCCCC	CAGCAGAGTC	ATTGAATGG?	AGTTAAGATGG	AGTTG
TrMDHb3	:	CTTCACATGCTTGA	TATECCTCCAC	CAGCAGAGTC	ATTGAATGG	agttaa <mark>a</mark> atgg:	AGTTG
TrMDHb4	:	CTTCACATGCTTGA	TATCCCTCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAXATGG	AGTTG
TrMDHb5	:	CTTCACATGCTTGA					
TrMDHb6	:	CTTCACATGCTTGA	TATCCCTCCAG	CAGCAGAGÑC	ATTGAATGG	\GTTAAÄATGG	AGTTG
TrMDHb7	:	CTTCACATGCTTGA					
TrMDHb8	. :	CTTCACATGCTTGA	TATECCTCCAC	CAGCAGAGTC	ATTGAATGG	AGTTAAAATGG	AGTTG
TrMDHb9	:	CTTGACATGCTTGA	TATTGCT@CAG	NAGNAGAGTÑ	ATTGAATGG	AGCTAAAATGG	AGETG
TrMDHb10	:	CTACACATGCTTGA	TATTCCÄCCCG	CAGCAGAGTC	ATTGAATGG/	AGTTAAGATGG?	AGTTG
TrMDHb11	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAGATGG	AGTTG
TrMDHb12	:	CTÄCACATGCTTGA	TATTCCÄCCÜG	CAGCAGAGTC	ATTGAATGG	AGTTAAGATGG	AGTTG
TrMDHb13	:	CTTCACATGCTTGA	TATCCTCCAG	CAGCAGAGTC	ATTGAATGG	agttaa¤atgg:	AGTTG
TrMDHb14	:	CTTCACATGCTTGA					
TrMDHb15	:	CTACACATGCTTGA	TATTCCÁCCÉG	CAGCAGAGTCA	ATTGAATGG	AGTTAAGATGG	AGTTG
TrMDHb16	:	CTACACATGCTTGA					
TrMDHb17	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAAT <b>G</b> G	agttaa <u>R</u> atgg	AGTTG
TrMDHb18	:	CTTCACATGCTTGA					
TrMDHb19	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAAAATGG	AGTTG
TrMDHb20	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAMATGG	AGTTG
TrMDHb21	:	CTTCACATGCTTGA					
TrMDHb22	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAAAATGG	AGTTG
TrMDHb23	:	CTACACATGCTTGA					
TrMDHb24	:	CTACACATGCTTGA					
TrMDHb25	:	CTTCACATGCTTGA					
TrMDHb26	:	CTTCACATGCTTGA	TATTCCTCCAG	CAGCAGAGTC	ATTGAATGGA	AGTTAA!A!ATGG!	AGTTG
TrMDHb27	:	CTTCACATGCTTGA	TATICITCCAG	CAGCAGAGTC	ATTGAATGG	AGTTAAGATGG	AGTTG
TrMDHb28	:		TATECCTCCAG				
TrMDHb29	:		TATTCCTNCMG				
TrMDHb30	:		TATTCCT-CCG	CAGCAGAGT-	ŅTTGAATGG <i>A</i>	G-TAAGATGG	AGTTG
TrMDHb31	:						
TrMDHb32	:						

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		* 320	*	340 .	*	360		
TrMDHb1	:	GNCGATGCTGNATTNNCACTTGTT	AAAGGMGANG	CTGCT			:	323
TrMDHb2	:	GTCGATGCTGCATTTCCACTTGTT	TAAAGGTGNTG	<b>MTGNTACAACT</b>	GATGATGEN	GAĞGNA	:	342
TrMDHb3	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACT	GATGTTGTT	GAAGCA	:	334
TrMDHb4	:	GTËGATGCTGCATTTCCACTTCTT	PAAAGG GTTG	TTGCTACAACT	GATGTTGTT	GAAGCA	:	331
TrMDHb5	:	GTCGATGCTGCATTTCCACTTCTT	AAAGGTGTTG	TTGCTACAACT	GATGTTGTT	GAGGCA	:	331
TrMDHb6	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGĞGTTG	TTGCTACAACT	GATGTTGTT	GAAGCA	:	324
TrMDHb7	:	GCGGATGCTGCATTTCCACTTCTT					:	325
TrMDHb8	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGCGTTG	TTGCTACAACI	CATGTTGTT	GAAGCA	:	324
TrMDHb9	:	CCGGATGCTGNATTNNAACTTCTT	Pagagggg <mark>g</mark> g	CCGCTACCACI	GATG TGC	CAACCA	:	312
TrMDHb10	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTC	TTGCTACAACI	GATGTTGTT	GAGGCA	:	318
TrMDHb11	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACT	GATGTTGTT	GAGGCA	:	320
TrMDHb12	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACT	GATGTTGTT	GAGGCA	:	321
TrMDHb13	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGG[CGTTC	TTGCTACAACT	GATGTTGTT	'GAAGCA	:	315
TrMDHb14	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACT	GATGTTGTT	'GAAGCA	:	311
TrMDHb15	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTC	TTGCTACAACI	GATGTTGTT	GAGGCA	:	319
TrMDHb16	:	GTCGATGCTGCATTTCCACTTCTT					:	318
TrMDHb17	:	GTGGATGCTGCATTTCCACTTCTT					:	316
TrMDHb18	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACI	GATGTTGTT	GAGGCA	:	314
TrMDHb19	:	GTGGATGCTGCATTTCCACTTCTT	PAAAGGTGTTC	TTGCTACAACI	GATGTTGTT	'GAAGCA	:	310
TrMDHb20	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGTGTTC	TTGCTACAACT	GATGTTGTT	GAAGCA	:	303
TrMDHb21	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTC	TTGCTACAACT	GATGTTGTT	GAGGCA	:	303
TrMDHb22	:	GTGGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACI	GATGTTGTT	GAAGCA	:	299
TrMDHb23	:	GTCGATGCTGCATTTCCACTTCTT	TAAAGGTGTTG	TTGCTACAACI	GATGTTGTT	GAGGCA	:	290
TrMDHb24	:	GTCGATGCTGCATTTCCACTTCTT					:	289
TrMDHb25	:	GTCGATGCTGCATTTCCACTTCTT				the st	:	286
TrMDHb26	:	GTGGATGCTGCATTTCCACTTCTT				T1001	:	283
TrMDHb27	:	GTCGATGCTGCATTTCCACTTCTT					:	277
TrMDHb28	:	gt@gatgctgcatttccacttctt	raaagg <u>ca</u> tto	TTGCTACAACI	GATGTTGTT	GAAGCA	:	153
TrMDHb29	:	GTCGATGCTGCATTTCCACTTCTT	PAAAGGTGTTC	STTGCTACAACT	GATGTTGTT	'GAGGCA	:	105
TrMDHb30	:	GTCGATGCTGCATTTCC-CTTCTT	PAAAGGTGTTC	STTGCTACAACT	GATGTTGTT	GAGGCA	:	102
TrMDHb31	:						:	_
TrMDHb32	:			<i></i>			:	-

400 380 TrMDHb1 TrMDHb2 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 394 TrMDHb3  ${\tt TGCACTGGAGTCAATATTGCAGTCATGGTTGGT}{\tt GGATTCCCAAGAAAAGAAGGTATGGAG}$ 391 TrMDHb4 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 391 TYMDHb5 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 384 TrMDHb6 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 385 TrMDHb7 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 384 TrMDHb8 TGCGCTGCA-CCGATATMCCMN----TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAN 333 TrMDHb9 378 TrMDHb10 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 380 TrMDHb11 381 TrMDHb12 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 375 TrMDHb13 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 371 TrMDHb14 : TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG TGCACTGGAGTCAATATCGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 379 TrMDHb15 378 TrMDHb16 : : 376 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG TrMDHb17 : : 374 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG TrMDHb18 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGCTATGGAG : 370 TrMDHb19 : 363 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTÑTGGAG TrMDHb20 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 363 TrMDHb21 : 359 TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : TrMDHb22 : : 350 TrMDHb23 : : 349 TrMDHb24 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 346 TrMDHb25 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 343 : TrMDHb26: TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 337 TrMDHb27: TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 213 TrMDHb28: TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 165 TrMDHb29 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG 162 TrMDHb30 : TrMDHb31 : TrMDHb32:

420

460 480 440 TrMDHb1 TrMDHb2 AGGAAGGATGTGATGACTAAGAAÏGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA AGGAAGGATGTGATGACTAAGAAÏGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA TrMDHb3 451 TrMDHb4 AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 451 TrMDHb5 AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 444 TrMDHb6AGGAAGGATGTGATGÄCTAAGAA 445 TrMDHb7 AGGAAGGATGTGATGACTAAGAAHGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 444 TrMDHb8 TrMDHb9 438 AGGAAGGATGTIJATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA TrMDHb10 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 440 TrMDHb11: AGGAAGGATGTÏATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 441 TrMDHb12 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA AGGAAGGATGTGATGACTAANAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 435 TrMDHb13 : : 431 TrMDHb14 : AGGAAGGATGTÄATGTCTAAGAACGTCTCTATTTACAAGTCCCAÄGCTTCTGCCCTTGAA 439 TrMDHb15 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA 438 TrMDHb16: AGGAAGGATGTGATGÄCTAAGAAÜGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 436 TrMDHb17: 434 AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA TrMDHb18: AGGAAGGATGTGATGÄСТААGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA AGGAAGGATGTGATGÄCTAAGAÑTGTCTCTATTTACAA<u>ÑANNÑ</u>AGÑCTTÑTGÑCCTTGAA 430 TrMDHb19: 423 TrMDHb20: AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 423 TrMDHb21: AGGAAGGATGTGATGڲCTAAGAAjjGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 419 TrMDHb22 : aggaaggatgtijatgtctaagaacgtctctatttacaagtcccaagcttttgcccttgaa : 410 TrMDHb23: AGGAAGGATGTLATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 409 TrMDHb24 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 406 TrMDHb25 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 403 TrMDHb26 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 397 TrMDHb27: : 273 AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA TrMDHb28: : 225 AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA TrMDHb29 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 222 TrMDHb30 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA 64 TrMDHb31 : 64 МҊ҉ҫӎ҉҇ѧӎ҉҄ҫӎ҅҃ӎ҈ҁтgatgtctaaӎ҉аасgtctctatttacaagtcccaggcttctgcccttgaa

TrMDHb32 :

500 520 540 TrMDHb1 TrMDHb2 TrMDHb3 AAGCATGCTGCCAACTGCAAGGTTTTTGGTTÄTTGCTAACCCAGCAAA AAGCATGCTGCCAACTGCAAGGTTTTGGTTÄTTGCTAACCCAGCAAAMACCAATGCA AAGCATGCTGCCGAACTGCAAGGMTTTGGTTGMTGCTAACCCAMCAACACCAATGCA TrMDHb4 : 511 TrMDHb5 : 510 AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA TrMDHb6 AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTT : 504 TrMDHb7 TTGCTAACCCAGCAAAIIACCAATGCA : 505 TrMDHb8 AAGCATGCTGCCAACTGCAAGGTTTTGGTTÄTTGCTAACCCAGCAAATACCAATGCA : 504 TrMDHb9 TrMDHb10 :  ${ t AAGCATGCTGCCAACTGCAAGGTTTTGGTTGCTAACCCAGCAAACACCAATGCA}$ : 498 TrMDHb11 : AAGCATGCTGCCGAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA : 499 TrMDHb12: AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 501 TrMDHb13 aagcatgctgccaactgcaaggttttggttättgctaacccagcaaaiiaccaatgca : 495 TrMDHb14 : AAGCATGCTGCCAACTGCAAGGTTTTGG----462 TrMDHb15 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 499 TrMDHb16 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 498 ААGCATGCTGCCAACTGCAAGGÄTTTGGĜTÄTTGCTAACCCAÄCAAAĨĴACCAATGCA TrMDHb17: 496 TrMDHb18: AAGCATGCTGCCGAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA 493 TrMDHb19: AAGCATGCTGCCGCAACTGCAAGGTTTTGGTTÄTTGCTAACCCAGCAAAIACCAATGCA 490 TrMDHb20 : AAAGATNCTG-----433 TrMDHb21 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 483 TrMDHb22: AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTÄTTGCTAACCCAGCAAATACCAATGCA 479 TrMDHb23 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 470 TrMDHb24 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGCTAACCCAGCAAACACCAATGCA 469 TrMDHb25: AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 466 TrMDHb26 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTÄTTGCTAACCCAGCAAAÏACCAATGCA 463 TrMDHb27 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 457 aagca<u>a</u>gctgctgccaactgcaaggttttggtt<u>ä</u>ttgctaacccagcaaa<u>ii</u>accaatgca TrMDHb28 : : 333 AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA TrMDHb29: : 285 TrMDHb30 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 282 TrMDHb31 : AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA 124 AAGCATGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA TrMDHb32

		*	560	*	580	*	600		
TrMDHb1	:							:	-
TrMDHb2	:			·i				:	-
TrMDHb3	:		GGAGTTTGCTCCAT					:	574
TrMDHb4	:		.gga <mark>g</mark> tttgctccat	CTATTCCA	GAGAAAAACATT	TCAGCTTTGA	CTAGA	:	571
TrMDHb5	:	TTGATCTTGNA						:	531
TrMDHb6	:	TTGATCTTGAA	.GGAGTTTGCTCCAT	CTATTCCA	GAGAAAAACATT	TCAGCTTTGA	CTAGA	:	564
TrMDHb7	:		.GGAGTTTGCTCCAT					:	565
TrMDHb8	:	TTGATCTTGAA	.GGAGTTTGCTCCAT	CTATTCCA	GAGAAAAACATT	TCAGCTTTGA	CTAGA	:	564
TrMDHb9	:							:	-
TrMDHb10	:		GGAATTTGCTCCAT					:	558
TrMDHb11	:	TTGATCTTGAA	GGAATTTGCTCCAT	CTATTCCA	GAGAAAAACATI	TCTTGTTTGA	CTAGA	:	559
TrMDHb12	:		GGAATTTGCTCCAT					:	561
TrMDHb13	:	TTGATCTTGAA	.GGAĞTTTGCTCCAT	CTATTCCA	GAGAAAAACATI	TCAGCTTTGA	CTAGA	:	555
TrMDHb14	:							:	_
TrMDHb15	:	TTGATCTTGAA	GGAATTTGCTCCAT	CTATTCCA	GAGAAAAACATI	TCTTGTTTGA	CTAGA	:	559
TrMDHb16	:		GGAATTTGCTCCAT				CTAGA	:	558
TrMDHb17	:	TTGATCTTGAA	ggagtttgctccat	CTATTCCA	<sub>З</sub> А҈ÑАААААСАТТ	TCANCTTTG-		:	550
TrMDHb18	:		GGAATTTGCTCCAT					:	553
TrMDHb19	:	TTGATCTTGAA	gga@tttgctccat	CTATTCCA	GAGAAAAACATI	TCAGCTTTGA	CTAGA	:	550
TrMDHb20	:							:	-
TrMDHb21	:		GGAATTTGCTCCAT					:	543
TrMDHb22	:	TTGATCTTGAA	gga <u>ë</u> tttgctccat	CTATTCCAC	GAGAAAAACATI	TCAGCTTTGA	CTAGA	:	539
TrMDHb23	:	TTGATCTTGAA	GGAATTTGCTCCAT	CTATTCCA	GAGAAAAACATT	TCTTGTTTGA	CTAGA	:	530
TrMDHb24	:		GGAATTTGCTCCAT					:	529
TrMDHb25	€,		GGAATTTGCTCCAT					:	526
TrMDHb26	:		GGAĞTTTGCTCCAT					:	523
TrMDHb27	:		GGAATTTGCTCCAT					:	517
TrMDHb28	:		ggagtttgctccat					:	393
TrMDHb29	:		GGAATTTGCTCCAT					:	345
TrMDHb30	:	TTGATCTTGAA	GGAATTTGCTCCAT	CTATTCCAC	GAGAAAAACATT	TCTTGTTTGA	CTAGA	:	342
TrMDHb31	:		GGAATTTGCTCCAT					:	184
TrMDHb32	:	TTGATCTTGAA	GGAATTTGCTCCAT	CTATTCCAC	BAGAAAAACATT	TCTTGTTTGA	CTAGA	:	184
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TrMDHb1	:						- :	_
TrMDHb2	:						- :	_
TrMDHb3	:	CTTGATCACAA					·- :	585
TrMDHb4	:	CTTGATCACAACAGGGCA	TTGG				- :	593
TrMDHb5	:						- :	-
TrMDHb6	:	CTTGATCAC					- :	573
TrMDHb7	:	CTTGATCACAACAGGGCA	TTGGGCCAAAT	ITCTGAAA			- :	603
TrMDHb8	:	CTTGATCACAACAGGGCA	TTGGGCCAAATT	TTCT			- :	597
TrMDHb9	:						- :	
TrMDHb10	:	CTTGATCAC					- :	567
TrMDHb11	:	CTTGATCACC					- :	569
TrMDHb12	:	CTTGATCACAACAGGGCA	TTGGGCCAAATT	W			- :	592
TrMDHb13	:	CTTGATCACAACAGGGCA					_ ;	585
TrMDHb14	:						_ :	-
TrMDHb15	:	CTTGATCACAACAG					- :	573
TrMDHb16	:	CTTGATCACAACAGGGCA	TTGGGCCAAATT	TCTGAAAC	ATTGAAT		_ ;	603
TrMDHb17	:						- :	-
TrMDHb18	:	CTTGATCACAACAGGGCA	TTGGGCCAAATT	TCTGAAAG			- :	591
TrMDHb19	:	CTTGATCACAACAGGGCA	TTG				- :	571
TrMDHb20	:						- :	٠-
TrMDHb21	:	CTTGATCACAACAGGGCA					- :	585
TrMDHb22	:	CTTGATCACAACAGGGCA	TTGGGCCAAATT	TCTGAAAG	ATTGAATA'TTC	AAGTTTCTGA		599
TrMDHb23	:	CTTGATCACAACAGGGCA'	TTGGGCCAAATT	TCTGAAAG			- :	568
TrMDHb24	:	CTTGATCACAACAGGGCA					- :	558
TrMDHb25	:	CCTGATCACAACAGGGCA'	TTGGGCCAAATT	TCTGAAAG	ATTGAATGTTC	AAGTTTCTGA	T:	586
TrMDHb26	:	CTTGATCACAACAGGGCA'	TTGGGCCAAATT	TCTGAAAG	ATTGAATATTC	AAGTTTCTGA	т :	583
IrMDHb27	:	CTTGATCACAACAGGGCA'	TTGGGCCAAATT	TCTGAAAG	SATTGAATGTTC	AAGTTTC	- :	573
TrMDHb28	:	CTTGATCACAACAGGGCA	ITG <u>G</u> GCCAAAT1	TCTGAAAG	ATTGAATÄTTC	AAGTTTCTGA	1 :	453
TrMDHb29	:	CTTGATCACAACAGGGCA'	ITGNGCCAAATT	TCTGAAAG	ATTGAATGTEC	AAGTTTCTGA	<u> </u>	405
TrMDHb30	:	CTTGATCACAACAGGGCA'	<b>TTGGGCCAAATT</b>	TCTGAAAG	ATTGAATGTCC	AAGTTTCTGA	r :	402
rmDHb31	:	CTTGATCACAACAGGGCA:	FTGGGCCAAATT	TCTGAAAG	ATTGAATGTTC	AAGTTTCTGA	T :	244
rmDHb32	:	CTTGATCACAACAGGGCA:	ITGGGCCAAATT	TCTGAAAG	ATTGAATGTTC	AAGTTTCTGA	:	244

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		*	680	*	700 .	*	720	
TrMDHb1	:							: .
TrMDHb2	:							: .
TrMDHb3	:							: .
TrMDHb4	:							: .
TrMDHb5	:							: .
TrMDHb6	:							: '
TrMDHb7	:							: .
TrMDHb8	:							: .
TrMDHb9	:							: .
TrMDHb10	:		_					: 4
TrMDHb11	:							: .
TrMDHb12	:							: .
TrMDHb13	:							: '
TrMDHb14	:							: .
TrMDHb15	:							:
TrMDHb16	:							: .
TrMDHb17	:							:
TrMDHb18	:							:
TrMDHb19	:							:
TrMDHb20	:							:
TrMDHb21	:							
TrMDHb22	:	GTAAAGAATGT						: 61
TrMDHb23	:							:
TrMDHb24	:							:
TrMDHb25	:	GTAAAGAATGTCATTA	TCTGGGGTAATC	ATTCATCA	ACTCAGTATCCT	GATGTCAA	CCAT	: 64
TrMDHb26	:							:
TrMDHb27	:							:
TrMDHb28	:	GTAAAGAATGTCATTA						: 51
TrMDHb29	:	GTAAAGAATGTCATTA						: 46
TrMDHb30	:	GTAAAGAATGTCATTA						: 46
TrMDHb31	:	GTAAAGAATGTCATTA	ATCTGGGGTAATC	ATTCATCA	ACTCAGTATCCT	GATGTCAA	CCAT	: 304
TrMDHb32		GTAAAGAATGTCATT	TOTA ATO	ATTCATCA	ACTCAGTATCCT	GATGTCAA	CCAT	: 304

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		* 740	•	760		
TrMDHb1			*	760	*	780
TrMDHb2	:		<del>-</del> -			
TrMDHb3	:					
TrMDHb4	:					
TrMDHb5	:					
TrMDHb6	•					
TrMDHb7	:					
TrMDHb8	:					
TrMDHb9	:					
TrMDHb10	•					
TrMDHb11	:					
TrMDHb12	:					
TrMDHb13	:					
TrMDHb14	:					
TrMDHb15	:					
TrMDHb16	•					
TrMDHb17	:					
TrMDHb18	:					
TrMDHb19	:					
TrMDHb20	:					
TrMDHb21	:					
TrMDHb22	:					
TrMDHb23	:					
TrMDHb24	:					
TrMDHb25	:	GCAACTGTTAACACCCCCGCTGG	GGAGAAGCCTG	тесетелестт	CTTTCTC AT	ZA CCCC
TrMDHb26	:					SACGCC
TrMDHb27	:					
TrMDHb28	:	GCAACTGTTAACACCCCCGC@GG	GGAGAAGCCTG	TCCGTGAACTT	CTTTT	
TrMDHb29		GCAACTGTTAACACCCÄCGCTGÄ	NGAGAAGCCTC	TCCGTGAGCTI	CTTT	·
TrMDHb30	:	GCAACTGTTAACACCCCCGCTGG	GGAGAAGCCTG	TCCGTGAGCT <u>M</u>	CTTTCTCATC	TA CCCC
TrMDHb31	:	GCAACTGTTAACACCCCCGCTGG	GGAGAAGCCTG	TCCGTGAGCTT	CTTTCTGAT	GACGCC
TrMDHb32	:	GCAACTGTTAACACCCCCGCTGG	GGAGAAGCCTG	TCCGTGAGCTT	GTTTCTGAT GTTTCTGAT	PACGCC

		*	800	*	820	*	840		
TrMDHb1	:							:	-
TrMDHb2	:•							:	_
TrMDHb3	:							:	_
TrMDHb4	:							•	_
TrMDHb5	:							•	-
TrMDHb6	:							:	_
TrMDHb7	:							:	_
TrMDHb8	:							•	-
TrMDHb9	:							:	_
TrMDHb10	:							•	-
TrMDHb11	:							:	_
TrMDHb12	:							•	_
TrMDHb13	:			4				•	_
TrMDHb14	:							•	_
TrMDHb15	:								_
TrMDHb16	:							•	_
TrMDHb17	:		·						· _
TrMDHb18	:							:	_
TrMDHb19	:							:	_
TrMDHb20	:				:			:	-
TrMDHb21	:							:	_
TrMDHb22	:							:	_
TrMDHb23	:							:	_
TrMDHb24	:							:	_
TrMDHb25	:	TGGTTGAATGGAG	AATTCATATCTAC	CGTTCAA	CAACGTGGTGCTC			:	752
TrMDHb26	:							:	_
TrMDHb27.	:							:	_
TrMDHb28	:							:	_
TrMDHb29	:							:	-
TrMDHb30	2	TGGTTGAATGGAGA	ATTCATATCTAC	CGTTCAA	CAACGTGGTGCTG	CAATTATTA	AGGCT	:	582
TrMDHb31	:	TGGTTGAATGGAGA	ATTCATATCTAC	CGTTCAA	CAACGTGGTGCTG	CAATTATTA	AGGCT	:	424
TrMDHb32	:	TGGTTGAATGGAGA	ATTCATATCTAC	CGTTCAA	CAACGTGGTGCTC	CAATTATTA	AGGCT	:	424
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				0.00	*	880	*	900		
			*	860	•					_
TrMDHb1	:					· · · · · · · · · · · · · · · · · · ·			•	_
TrMDHb2	:								•	_
TrMDHb3	:								•	_
TrMDHb4	:									_
TrMDHb5	:	·							•	_
TrMDHb6	:								•	_
TrMDHb7	:								:	_
TrMDHb8	:								:	-
TrMDHb9	:				_				:	-
TrMDHb10	:						•		:	-
TrMDHb11	:								:	-
TrMDHb12	:				<del></del>			<del>-</del>	:	-
TrMDHb13	:								:	-
TrMDHb14	:								:	-
TrMDHb15	:								:	-
TrMDHb16	:								:	-
TrMDHb17	:		,						:	-
TrMDHb18	:								:	-
TrMDHb19	:								:	-
TrMDHb20	:								:	-
TrMDHb21	:								:	-
TrMDHb22	:								:	-
TrMDHb23	:								:	-
TrMDHb24	:								:	-
TrMDHb25	:								:	-
TrMDHb26	:								:	-
TrMDHb27	:								:	-
TrMDHb28	:								:	-
TrMDHb29	:								:	
TrMDHb30	:	AGAAAGCT"	TCAAGEG						:	598
TrMDHb31	:	AGAAAGCT'	TCAAGCG	CACTATCCGCTG	CTAGCGCT	GCTTGCGACCAC.	ATTCGCGA	TTGG	:	484
TrMDHb32	:	AGAAAGCT"	TCAAGCG	CACTATCCGCTG	CTAGCGCT	GCTTGCGACCAC	ATTCGCGA	TTGG	:	484

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		*	920	*	940	*	960			
TrMDHb1	:							•	_	
TrMDHb2	:							:	_	
TrMDHb3	:							:	_	
TrMDHb4	:							•	_	
TrMDHb5	:							•	_	
TrMDHb6	:							•	_	
TrMDHb7	:							•	_	
TrMDHb8	:							:	_	
TrMDHb9	:							•	-	
TrMDHb10	:							:	_	
TrMDHb11	:							:	-	
TrMDHb12	:							:	_	
TrMDHb13	:							:	_	
TrMDHb14	:							:	_	
TrMDHb15	:							:	_	
TrMDHb16	:							:	_	
TrMDHb17	:							:	_	
TrMDHb18	:							:	-	
TrMDHb19	:							į	_	
TrMDHb20	:							:	-	
TrMDHb21	:							:	_	
TrMDHb22	:							:	-	
TrMDHb23	:							:	-	
TrMDHb24	:							:	-	
TrMDHb25	:					•		:	-	
TrMDHb26	:							:	-	
TrMDHb27	:							:	-	
TrMDHb28	:							:	-	
TrMDHb29	:							:	-	
TrMDHb30	:							:	-	
TrMDHb31	:	GTTCTTGGAACTCCCC	AGGGCACCTTCGT	'TTCAATGG	GAGTGTATTCTG	ATGGTTC:	TTAC	:	544	
TrMDHb32	:	GTTCTTGGAACTCCCC	AGGGCACCTTCGT	TTCAATGG	GAGTGTATTCTG	ATGGTTC'	<b>LTAC</b>	:	544	

(FreMDIVI) 7		* 980 <sub>.</sub>	*	1000	*	1020		
TrMDHb1	:						:	-
TrMDHb2	:					,	:	-
TrMDHb3	:						:	-
TrMDHb4	:						:	-
TrMDHb5	:						:	-
TrMDHb6	:						:	-
TrMDHb7	:						:	-
TrMDHb8	:						:	-
TrMDHb9	:						:	-
TrMDHb10	:						:	-
TrMDHb11	:			:			:	-
TrMDHb12	:						:	-
TrMDHb13	•						:	_
TrMDHb14	:						:	-
TrMDHb15	:						:	-
TrMDHb16	:						:	-
TrMDHb17	:						:	-
TrMDHb18	:						:	-
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TrMDHb21	:						:	-
TrMDHb22	:						:	-
TrMDHb23	:						:	-
TrMDHb24	:						:	-
TrMDHb25	:						:	-
TrMDHb26	:						:	-
TrMDHb27	:						:	-
TrMDHb28	:						:	-
TrMDHb29	:						:	-
TrMDHb30	:						:	-
TrMDHb31	:	AACGTACCAGCTGGACTCATCTA					:	603
TrMDHb32	:	AACGTACCAGCTGGACTCATCT	ATTCATTCCCTC	TCACCACTGC'	TAATGGGGAAT	CGGAAA	, <b>:</b> `	604

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		*	1040	*	1060	*	1080		
TrMDHb1 :	:								_
TrMDHb2 :					•			:	_
TrMDHb3 :								:	_
TrMDHb4 :								:	_
TrMDHb5 :								:	٠
TrMDHb6 :								:	_
TrMDHb7 :								:	_
TrMDHb8 :								:	_,
TrMDHb9 :								:	_
TrMDHb10 :								:	_
TrMDHb11 :								:	_
TrMDHb12 :								:	_
TrMDHb13 :								:	_
TrMDHb14 :								:	_
TrMDHb15 :								:	_
TrMDHb16 :								:	_
TrMDHb17 :								:	_
TrMDHb18:								:	_
TrMDHb19 :								:	_
TrMDHb20 :								:	_
TrMDHb21 :								•	•••
TrMDHb22:				<b></b>				•	_
TrMDHb23:								:	_
TrMDHb24 :						1		:	_
TrMDHb25 :								:	_
TrMDHb26 :								:	-
TrMDHb27 :								:	-
TrMDHb28:						. <b></b>		:	-
TrMDHb29:								:	-
TrMDHb30 :								:	-
TrMDHb31 :								:	-
TrMDHb32:	ATTG	TTCAAGGAC:	TTTCAATTGACG	AGTTCTCAA	GGAAGAAGTTG	GACTTGACAG	CTGAA	:	664

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		*	1100		
TrMDHb1	:			·	
·TrMDHb2	:				
TrMDHb3	:				
TrMDHb4	:				: -
TrMDHb5	:				
TrMDHb6	:				
TrMDHb7	:				
TrMDHb8	:				· -
TrMDHb9	:				
TrMDHb10	:				
TrMDHb11	:				•
TrMDHb12	:				: -
TrMDHb13	:				: -
TrMDHb14	:				: -
TrMDHb15	:				: -
TrMDHb16	:				: -
TrMDHb17	:				: -
TrMDHb18	:				: -
TrMDHb19	:				: <del>-</del>
TrMDHb20	:				: -
TrMDHb21	:				: - : -
TrMDHb22	:	·- <del>-</del>			: - : -
TrMDHb23	:				: -
TrMDHb24	:				· -
TrMDHb25	:				•
TrMDHb26	:				-
TrMDHb27	:				=
TrMDHb28	:				
TrMDHb29	:				. <del>-</del>
TrMDHb30	:				_
TrMDHb31	:				A -
TrMDHb32	: GAGTTATC	CGAGGAA	AAGAGTTTGG	CATACT :	695
					093

TrMDHc	: <b>:</b>	* 20 * 40 * 60 AAAGNGAATTGGAATATACGACACTCCATTCCATACTTCCATTCCTTTCTC	:	60
TrMDHc	:	* 80 * 100 * 120 GCTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAATTATGAGG	:	120
TrMDHc	:	* 140 * 160 * 180 CCGTCGATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGC	:	180
TrMDHc	:	* 200 * 220 * 240 CGTGGCTATGCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGC	:	240
TrMDHc	:	* 260 * 280 * 300 GGGATCGGCCAGCCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCT	:	300
TrMDHc	:	* 320 * 340 * 360 CTTTATGATATTGCTGGAACCCCTGGTGTCGCCGCTGATGTCAGCCCACATCAACTCCAGA	<b>:</b> -	360
TrMDHc	:	*. 380 * 400 * 420 TCTGAGGTAACTGGGTATGCAGGTGAAGAGGCTTTGGAAGAGGTGCTGAT	:	420
TrMDHc	:	* 440 * 460 * 480 GTTGTTATAATTCCTGCTGGTGTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTC	:	480
TrMDHc	:	* 500 * 520 * 540 AATATTAACGCTGGCATTGTCAAGTCACTTGCCACTGCTATTTCTAAGTACTGCCCCCAT	:	.540
TrMDHc	:	* 560 * 580 * 600 GCCCTTGTTAACATGATAAGCAACCCTGTGAACTCCACCGTTCCCATTGCTGCAGAGGTT	:	600
TrMDHc	:	* 620 * 640 * 660 TTCAAGAAGGCAGGGACATATGACGAGAAGAGATTGTTTGGGGTTACAACCCTTGATGTA	:	660
TrMDHc	:	* 680 * 700 * 720 GTCAGGGCAAAAACTTTCTATGCCGGGAAAGCTAAAGTTCCAGTTGCCGAGGTCAATGTA	:	720
TrMDHc	:	* 740 * 760 * 780 CCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTTCCATTATTTTNTCAGGCAACACCT	:	780
TrMDHc	:	* 800 * 820 * 840 CAAGCCAATCTGGGTGATGATACCCTTAAGGNTTTAACGGNANGGACACAAGATGGAGGA	:	840
TrMDHc	:	* 860 * 880 * 900 ACAGAAGTTGNGACCGCCAAGGCTGGAAAGGGTTCTGCAACTTTGTCAATGGCTTATGCT	:	900
TrMDHc	:	* 920 * 940 * 960 GGAGCCATATTTGCTGATGCTNGCCTCAAAGGNCTGAATGGAGTTCCAGATGTTATTGAG:	ŧ	960

\* 1060 TrMDHc : ATTGGGAAGAATGGTGTGGAAGAAATTCTGGGGCTTAGGTTCTCTCACAGATTTCGAGCAA : 1080 \* . 1120 TrMDHc : CAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATCAAATTT : 1140 TrMDHc : GCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTTCCATTTAGAACCAGATCAA : 1200 TrmDHc : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTTAGG : 1320 TrMDHc : TTGGCCTTTCCATTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAA : 1380

\* 1400

TrMDHc : GGGTGNTGGNCANCGATACACANCCCCC : 1408

		* . 20		
TrMDHc	:	MRPSMLRSVQSAVSRASSHLTRRGYATEPVPERKVAILGAAGGIGQPLSLLMKLNPLVST	:	60
TrMDHc	:	* 80 * 100 * 120 LSLYDIAGTPGVAADVSHINSRSEVTGYAGEEELGKALEGADVVIIPAGVPRKPGMTRDD	:	120
TrMDHc	:	* 140 * 160 * 180 LFNINAGIVKSLATAISKYCPHALVNMISNPVNSTVPIAAEVFKKAGTYDEKRLFGVTTL	:	180
TŕMDHc	:	* 200 * 220 * 240 DVVRAKTFYAGKAKVPVAEVNVPVIGGHAGVTILPLFXQATPQANLGDDTLKXLTXXTQD	:	240
TrMDHc	:	* 260 * 280 * 300 GGTEVXTAKAGKGSATLSMAYAGAIFADAXLKXLNGVPDVIECSYVQSNIISDLPFFASK	:	300
TrMDHc	:	* 320 * 340 VRIGKNGVEEILGLGSLTDFEQQGLENLKAELKSSIEKGIKFASQ : 345		

onsensus contig sequence TrMDHc

		* 20 * 40 * 60		
TrMDHc1	:	AAAGNGAATTGGAATNT-CGAC-CTCCATTCCNTACT-THATTICATICNTCGCTCTCTCTCT	:	60
TrMDHc2	:	GINNATTGGAATATACNCCACTCCATTCCATACT-THATTICATICATCCATCGCTCTCTCT	:	59
TrMDHc3	:	GNNCATCGA-CACTCCCTACTTTCCTTACTTTTATCGCT	:	42
TrMDHc4	:	GMACT CCATTCCNTACTTN TTN TN TO TO TO THE TOTAL CONTACT TO THE TOTAL CONT	:	30
TrMDHc5	:		:	27
TrMDHc6	:	CNTCCAT@CCNTACTTT-NTTCNTCGCT	:	27
TrMDHc7	:		:	27
TrMDHc8	:	TCCCATTCCNTACTTTNTTTMTCG	:	27
TrMDHc9	:	TCCATTCCNTACTCT_ATTINTCGCT	:	25
TrMDHc10	:	TCC-TTCCATACTTT ATTICATED	:	25
TrMDHc11	:	***************************************	:	-
TrMDHc12	:		:	-
TrMDHc13	:		:	-
TrMDHc14	:	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	:	-
TrMDHc15	:		:	-
TrMDHc16	:	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	:	-
TrMDHc17	:		:	-
TrMDHc1		* 80 · * 100 * 120		
TrMDHc1		CTCTCTCTTTTATTCTCGAAAAGCTTCTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG	:	122
TrMDHc3	•	CTCTCTCT-T-TATTCTCGAAAAGCTTTTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG	:	119
TrMDHc3		CTCTCTCTTTTATTCTCGAAAAGCTTTTTCAGCCAIICAACGGAGAATTATGAGIICCGTCG	:	105
TrMDHc5	:	CTCTCTCTCTGTATTCTCGAAAAGCTTTTTCAGCCAACAACGAGAGAATAATGAGGCCGTCGCTCTCTCT	:	91
TrMDHc6	•	CTCTCTC TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGTTATGAGGCCGTCG CTCTCTC TTTATTCTCGAAAAGCTTTTT AGCCAACAACGGAGAGAATTATGAGGCCGTCG	:	88
TrMDHc7	•	CTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG	:	87
TrMDHc8	•	CTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAATÄATGAGGCCGTCG CTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACG—AGAGAATÄATGAGGCCGTCG	:	90
TrMDHc9		CTCTCTCTTTATTCTCGAAAAGCTTTTT-NGCCAACAACGAGAGAATAATGAGGCCGTCG	:	89 87
TrMDHc10	:	CTCTCTC TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG	:	86
TrMDHc11	:		:	48
TrMDHc12	:	TTCTCAAAAGCTTTTT-AGCC-ACAACG-AGAGAA-AATGAGGCCGTCG	:	46
TrMDHc13	:	TTCTCG-AAAGCTTTTTCAGCC-ACAACGNANAGAATAATGAGGCCGTCG	:	48
TrMDHc14	:	MCAACOMAINACHAIMAIGAGGCCGICG	•	+0
TrMDHc15	:		•	_
TrMDHc16	:		:	_
TrMDHc17	:		•	_
			•	-
		<u>*</u> 140 * 160 * 180		
TrMDHc1	:	ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCCTCCTCTCACCTAACCCGCCGTGGCTAT ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCCTCCTCTCTCACCTAACCCGCCGTGGCTAT	:	185
TrMDHc2	:	ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT		182
TrMDHc3	:	ATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCGTCTCTCTC	:	168
TrMDHc4 ·	:	ATGCTCAGATCIGTCCAATCAGCCGTÄTCCCGCGCCTCETCTCACCTAACCCGCCGTGGCTAT	:	154
TrMDHc5	:	ATGLITCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCCGCCGTGGCTAT	:	151
TrMDHc6	:	ATG[]]TCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT	:	150
TrMDHc7	:	ATGUTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT	:	153
TrMDHc8	:	ATGCTCAGATCCGTCCAATCAGCCGT&TCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT	:	152
TrMDHc9	:	ATGUTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCCTCTTCTCACCTAACCCGCCGTGGCTAT	:	150
TrMDHc10	:	ATGUTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT	:	149
TrMDHc11	:	ATGITCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT	:	111
TrMDHc12	:	ATGCTCAGATC#GTCCAATCAGCCGT#TCCCGCGCCTCFTCTCACCTAACCCGCCGTGGCTAT  ATGCTCAGATC#GTCCAATCAGCCGT#TCCCGGGCCTCGTCTCACCTAACCCGCCGTGGGTAT  ATGCTCAGATC#GTCCAATCAGCCGT#TCCCGGGCCTCGTCTCACCTAACCCGCCGTGGGTAT	:	108
TrMDHc13	:	ATGCTCAGATC[I]GTCCAATCAGCCGTATCCCGGGCCTCGTCTCACCTAACCCGCCGTGGGTAT	:	111
TrMDHc14	:		:	-
TrMDHc15	:		:	-
TrMDHc16	:		:	-
TrMDHc17	:		:	-

		* 200 * 220 * 240 *		
TrMDHc1	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG:	_	48
TrMDHc2	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG:	_	45
TrMDHc3	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG		31
TrMDHc4	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGTCAG	_	17
TrMDHc5	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG:		14
TrMDHc6	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG:		13
TrMDHc7	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG:	_	16
TrMDHc8	:	GCTACCGAACCAGTTCCAGAACGCAGGGGTGGCCATTCTCGGTGCTGCTGGGGGGATCGGACCAG	_	15
TrMDHc9	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG:	2	13
TrMDHc10	:	GCTACCGAACCAGTTCCAGAACGCAAGGMGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG:	2	12
TrMDHc11	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGATCGGCCAG:	1	74
TrMDHc12	:	GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCTGGCGGGATCGGCCAG:	1	7:
TrMDHc13	:	GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG:	1	74
TrMDHc14	:	:		-
TrMDHc15	:			
TrMDHc16	:			
TrMDHc17	:			
	-	•		
		· · · · · · · · · · · · · · · · · · ·		
		260 * 280 * 300 *		
TrMDHc1	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	3	1:
TrMDHc2	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	_	01
TrMDHc3	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	-
TrMDHc4	:	CCTCTCTCTCTCATGAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	8
TrMDHc5	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	7
TrMDHc6	':	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	_	
TrMDHc7	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	-
TrMDHc8	:	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	
TrMDHc9	•	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:		-
TrMDHc10	•	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:		
TrMDHc11	•	CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	-
TrMDHc12		CCTCTCTCTCTCATGAAGCTCAAGCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT:	2	_
TrMDHc13		CCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT :		3,
TrMDHc14	•		~	_
TrMDHc15				
TrMDHc16	:			
TrMDHc17	:			
III DICI	•			Ī
		320 * 340 * 360 * 3		
TrMDHc1	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT :	3	74
TrMDHc2	:		3	・・ フィ
TrMDHc3	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:		<b>5</b> 7
TrMDHc4	•	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:	_	
TrMDHc5		GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT :	_	
TrMDHc6		GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:	3	
TrMDHc7	•	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:	3	
TrMDHc8	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:	3	
TrMDHc9		GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT:	3	
TrMDHc10	•	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT :		_
			3	
TrMDHc11	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT :	3	
TrMDHc12	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT :	2	
TrMDHc13	:	GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT	_	
TrMDHc14	:			54
TrMDHc15	:	GŅTGATGT-ŊGCC-CAT-AACTCC-GATCTGAGGTAACTGGGTAT:		4:
TrMDHc16	:			-
TrMDHc17	:	:		

		80 * 400 * 420 * 440		
rmDHc1	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	-	437
rmDHc2	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT		434
'rMDHc3	:	gcaggtgaagaagagcttggaaaagctttggagggtgctgatgttgttataattcctgc <u>g</u> ggt		420
rMDHc4	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	-	406
cMDHc5	:	gcaggtgaagaagagcttggaaaagctttggagggtgctgatgttgttataattcctgceeggt	-	403
rMDHc6	:	gcaggtgaagaagagcttggaaaagctttggagggtgctgatgttgttataattcctgc	-	402
rMDHc7	:	gcaggtgaagaagagcttggaaaagctttggagggtgctgatgttgttataattcctgc <u>c</u> ggt	-	405
rMDHc8	:	GCAGGTGAAGAAGACTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	:	404
rMDHc9	:	gcaggtgaagaagagcttggaaaagctttggagggtgctgatgttgttataattcctgc्2ggt	:	402
rMDHc10	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT	:	401
MDHc11	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGC <u>C</u> GGT	:	363
MDHc12	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	:	360
MDHc13	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	:	363
MDHc14	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	:	117
MDHc15	:	GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT	:	104
MDHc16	:		:	-
MDHc17	:		:	-
		·		
•		<u>* 460 * 480 * 500</u>		
MDHc1	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	500
MDHc2	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	497
MDHc3	:	gtgcccagaaagcctggaatgactcgtgatgatctttt   aatattaa   gctggcattgtcaag	:	483
MDHc4	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	469
MDHc5	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	466
MDHc6	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	465
MDHc7	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	468
MDHc8	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	467
MDHc9	:	gtgcccagaaagcctggaatgactcgtgatgatcttttcaatattaacgctggcattgtiiaag	:	465
MDHc10	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	464
MDHc11	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	426
MDHc12	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	423
MDHc13	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	426
MDHc14	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	180
MDHc15	:	GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG	:	167
MDHc16	:		:	_
MDHc17	:		:	-
•		. · · · · · · · · · · · · · · · · · · ·		
		* 520 * 540 * 560		
MDHc1	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATG	:	537
IDHc2	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT	:	560
4DHc3	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT	:	546
IDHc4	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT	:	532
IDHc5	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		529
MDHc6	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		528
MDHc7	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		531
IDHc8	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		530
IDHc9	•	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		528
MDHc10	:	TCACTTGCCACTGETATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		527
	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		489
MDHc12	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		486
	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		489
יים אנוועו	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT		243
		rementeeche tottal i i cimaline i dececci i di i i ancai da i and cade ce i		
MDHc13 MDHc14		₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽		
MDHc14 MDHc15	:	TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT	:	230
MDHc14		TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT	:	3

		*	580	*	600		*	620	*		
TrMDHc1	:									:	-
TrMDHc2	:	GTGAACTC	CACCGTTCCCATT	GCTG	CAGAGGTTT	TCAAGAAG	GCAGGG				608
TrMDHc3	:	GTGAACTC	CACCGTTCCCATI	CGCTG	CAGG						575
TrMDHc4	:	GTGAACTC	CACCGTTCCCATT	FGCTG	CAGAGG					_	563
TrMDHc5	:	GTGAACTC	CACCGTTCCCATT	rgctg	CAGAGGTTT	TCAAGAAG	GCAGGG	ACATAT		-	583
TrMDHc6		CTC A A CTC	CNCCCTTCCCCNT	rgctg	CAGAGGTTT	TCAAGAAG	GCAGGG	ACATATGAC	SAGAAG	-	591
TrMDHc7	:	GTGAACTC	CACCGTTCCCATT	rgctg	CAGAGGTTI	TCAAGAAC	GCAGGG	ACATATGAC	SAGAAG	-	594 556
TrMDHc8	:	CTCAACTC	CACCGTTCCCATT	rgctg	Q					-	556 591
TrMDHc9	:	GTGAACTC	CACCGTTCCCAT:	rgctg	CAGAGGTTI	TCAAGAA	3GC <u>A</u> GGG	ACATATGAC	JAGAAG	-	
TrMDHc10	:	CTCAACTC	CACCGTTCCCAT	TGCTG	NAGAGGTTI	TCAAGAA(	<b>3GCNGGG</b>	ACATATGAC	NAGAAN		590
TrMDHc11	:	CTCAACTC	CACCGTTCCCAT	TGCTG	CAGAGGTTT	TCAAGAA(	GCAGGC	ACATATGAC	GAGAAG	-	552
TrMDHc12	:	CTCDACTC	CACCCTTCCCAT	тсстс	CAGAGGTTT	TCAAGAA(	GCAGGG	ACATATGAC	GAGAAG	-	549
TrMDHc13	:	CTCAACTC	CACCGTTCCCAT'	TGCTG	CANAGGTTT	"TCAAGAA(	GGCAGGG	ACATATGAC	NAGAAG	-	552
TrMDHc14	:	CTCAACTC	CACCGTTCCCAT	TGCTG	CAGAGGTTI	TCAAGAA	GGCAGGG	ACATATGAC	GAGAIAG	-	306
TrMDHc15	:	GTGAACTC	CACCGTTCCCAT	TGCTG	CAGAGGTTT	TCAAGAA	GGCAGGG	ACATATGAC	GAGAAG	:	293
TrMDHc16	:									:	-
TrMDHc17	:									:	-
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TrMDHcl	:									:	_
TrMDHc2	:									•	_
TrMDHc3	:									•	_
TrMDHc4	:									•	_
TrMDHc5	:									:	598
TrMDHc6	:	AGATTGT-	TGGGGTTACAAC		27 0002 000	ACCCCCAA	א א כיתיתיתוֹי	TTATGCCGGG	AAAGCT	i	657
TrMDHc7	:	AGATTGT".	TTGGGGTTTACAAC	CCTTC	SATGTAGIC	AGGGC,GAM	MACIAI				_
TrMDHc8	:		TGGGGTTACAAC	00000		ACCCCGAA	እ እ <b>ር</b> ጥጥጥ	TATGCCGGG	AAAGCT	:	654
TrMDHc9	:	AGATTGT	rTGGGGTTACAAC rTGGGGTT <mark>-</mark> CAAC	CCTT	CAIGIAGIC	AADZDDDA 4 4 5 5 5 5 5 5	A A CTTT!	ที่วที่เรตccage	AAAGCT	:	652
TrMDHc10	•.	AAAT TGT	ITGGGGTTI-CAAC		GAIGIAGIC	accccan-	-1.C T T X		·	:	577
TrMDHc11	:	AGATTGT.	TTGGGGTTACAAC TTGGGGTTACAAC		CATCTACTC	ACCCAAA	AACT			:	594
TrMDHc12	:	AGATTGT	rTGGGGTTACAAC rTGGGGTTACAAC		CATCTACTIC.	AGGGCAAA	AACTTT	TTATGCILGGG	SAAAGCT	:	615
TrMDHc13	:	AGATTGT	rtggggttacaac rtggggttacaac		CATCTACEC.	AGGGCAAA	ידידים מ מ.	CTATGCTGGG	BAAAGCT	:	369
TrMDHc14	:	AGATTGT	I'IGGGGTTACAAC ITGGGGTTACAAC		GAIGIAGIC CATCTACTC	AGGGCAAA	AACTTT	CTATGCEGGG	BAAAGCT	:	356
TrMDHc15	:	AGA'I"I'G'I"	I'IGGGG I'IACAAC		GAIGIAGIC	AGGGGAA				:	_
TrMDHc16	:									:	_
TrMDHc17	:										
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TrMDHc1	:									:	_
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TrMDHc7	:	AAAGTTC	CAGTTGCCGAGG'	CAAT	GTACCTGT1	HTHGGAGC	SCCATGO	AGGAGIIAC.	TATTWIT		, 20
TrMDHc8	:									:	682
TrMDHc9	:	AAAGTTC	CAGTTGCCGAGG'	I'CAAT	GIAC	Nimirica ac		-NGAG-PNG	דאר דייי ביו	•	711
TrMDHc10		AAAGTTC	CAGTTGCCGNGG	SMAAT	.GINNCC.I.C.I.I	MITEGAG(	200-IIGC			•	
TrMDHc11										•	-
TrMDHc12						TATACCA C	2CC) TCC	ACCACTTAC	TATTCTX		678
TrMDHc13		AAAGTTC	CAGTTGCCGAGG	vCAA'I	GEACCIGII	ALAGGAG	TOO NOTOO	'AGGAGTTAC'	таттстс	,	432
TrMDHc14		AAAGTTC	CAGTTGCCGAGG	TCAA'I	GTACCTGTT	AIAGGAG	CCAIGC	'AGGAGTTAC'	TATTCTC		419
TrMDHc15		AAAGTTC	CAGTTGCCGAGG	TCAA'I	GIACCIGII	ALAGGAG	3CCA1GC			VI.	
TrMDHc16											_
TrMDHc17	7 ;									•	

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TrMDHc1		760 *	780		* 80	0	*	82	
TrMDHc1	:		- <b></b>					:	-
TrMDHc2	•							:	-
TrMDHc3	•							:	-
TrMDHcs	:							:	_
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TrMDHc6	:							:	
TrMDHc7	:	CCATTATTTTTTMAAGG-	AACACCTŅ	AAGCCAAT	VTGGMTGATG	BAAACCCTTA	IAGGNTTTAA	CG:	782
TrMDHc8	:							:	-
TrMDHc9	:							:	-
TrMDHc10	:	CCCTTHTTTTETHAGG-	ANNCCT-	NANCCANT	TNGGNGATN	IAAA - CCTTA	AAGGETTT-A	CC:	769
TrMDHc11	:							:	-
TrMDHc12	:							:	-
TrMDHc13	:	CCATTATTTTNTNAGGC?	ACACCT <u>N</u>	AAGCCAAT	VTGGGTGAWG	SATNCCCTTA	AGGNTTTAA	CG:	741
TrMDHc14	:	CCATTATTTTTTCAGGC	ACACCTC	AAGCCAAT	CTGGATGATG	SATACCATTA	AGGGTGTAA	CG:	495
TrMDHc15	:	CCATTATTTTTTCTCAGGC	ACACCTC	AAGCCAAT	CTGGÄTGATG	SATACCATTA	AGGCTCTAA	CG:	482
TrMDHc16	:		:					:	-
TrMDHc17	:							:	-
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TrMDHcl					860		880		_
TrMDHc2	:							:	_
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TrMDHc6	:							:	_
TrMDHc7	:	GNANGG CNCAAGATGG	GGAACÑG	AA-TTGNGA	ACCGCCAAGG	STT		:	827
TrMDHc8	:							:	_
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TrMDHc10	:	GE-NNGGCNCAAMANG-C	GGAACAA	AA-NTINGA	<u>C</u>			:	801
TrMDHc11	=							:	-
TrMDHc12	:							:	-
TrMDHc13	:	GNANGGAC <b>Ğ</b> CAA <b>Ğ</b> AÇĞGA	GGAACA	AANTTINGA	CCGCCANGG	-TGG-AAGG	GTTNT-NVA	CI:	801
TrMDHc14	:	GÖAÄGGACACAAGATGGA GÖAÄGGACACAAGATGGA	GGAACAG.	AAGTTG[[G/	ACCGCCAAGG	CTGGAAAGG	GTTCTGCAA	CT :	558
TrMDHc15	:	GGAAGACACAAGATGGA	GGAACAG	AAGTTG[[]GA	CCGCCAAGG	CTGGAAAGG	GTTCTGCAA	CI :	545
TrMDHc16	:							:	_
TrMDHc17	:							:	-
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TrMDHc1	:							;	_
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TrMDHc12	:							:	
TrMDHc13	:	TT- <u>ŅŅ</u> AATGGŸ						:	811
TrMDHc14	:	TTGTCAATGGCTTATGCT	GGAGCCA'	PATTTGCTG	ATGCTI GCC	TCAAAGGIC	TGAATGGAG	nn :	621
TrMDHc15	:	TTGTCAATGGCT						:	557
TrMDHc16	:			<u></u>	NTGCTNGCC'	T-NANGGNC	TGAATGGAG		34
TrMDHc17	:						GNGNG	rr :	7
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TrMDHc1 TrMDHc2	:							: -
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TrMDHc12	:							
TrMDHc13	•							
TrMDHc14		CCAGATGTTATTGAGTGCTCA	TATGTGC	ATCCAATATC	ТАТСТСТС	CCTTNCTT	тстттсст	: 684
TrMDHc15				AMICCAMIAIC	AICICIO		TCTTTCCT	
TrMDHc16		-CNGANGTTATTGAACTCTC	TATGTGC	ATCCAATATC	TATCTÁTC	CCTTCCTT	TCTTTGCT	: 96
TrMDHc17	:	-CMGAMGTTATTGAAGTCTCA CCAGATGTTATMGAGTGCT-	TATGTGC.	AT-CNATAT	NTCTCTG	ACCTTCCTT	TCTTTGCT	: 66
					MICIOIO.			
		* 1020	* :	1040	*	1060	*	
TrMDHcl	:							: -
TrMDHc2	:							: -
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TrMDHc5	:							: -
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TrMDHc14	:	TCCAAGGTGAGGATTGGGAA	AATGGTG.	I'GGGAANAA'I'				: 722
TrMDHC15	:	TCCAACCNINETCCATTCCCAAC		ccanaciano	eeme			. 770
TrMDHc17		TCCAAGG <u>NN</u> NGGATTGGGAAC TCC <mark>-</mark> AGGTGAGGATTGGGAAC				PACCETOTO	TCACACAT	: 138 : 128
II PIDITO I	•	TCC-AGGIGAGGAIIGGGAAC	MAIGGIG.	I GGAAGAAA I. J	CIGGGCI	IAGGIICIC	ICACAGAI	: 126
		1080 *	1100	,	• 11	L20	*	
TrMDHc1	:		·					: -
TrMDHc2	:		- <b></b>			·		: -
TrMDHc3	:							: -
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TrMDHc11	:							: -
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TrMDHc14 TrMDHc15	:							: -
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	:	TTCGAGCAACAAGGCCTTGAA	AACCTC	CCCROATCR			ACCCA A TIC	. 101
TTIMET!	•	I I COMOCAMCAAGGCCI I GAA	MAIACC I CAA	AGGCTGAACTC	AAATCATC	LAIIGAAA	AGGGAATC	: 191

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TrMDHcl	:							;	: -
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TrMDHc6	:							;	; <b>-</b>
TrMDHc7	:							:	: -
TrMDHc8	:							;	; -
TrMDHc9	:							:	-
TrMDHc10	:							:	-
TrMDHc11	:	_						:	-
TrMDHc12	-		_					:	-
TrMDHc13	:								-
TrMDHc14	:							:	-
TrMDHc15	:							:	-
TrMDHc16	:							:	-
TrMDHc17	:	AAATTTGCCTCCCAGT	AATCGAACATGT	CATACATT	ACTGGATTT	TTCCATTTA	GAACCAG	AT :	254
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TrMDHc1	:							:	<b>-</b>
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TrMDHc11	:							:	-
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TrMDHc14	•						<b>-</b>	:	-
TrMDHc15	:							:	-
TrMDHc16	:							:	-
TrMDHc17		CAAATTTTGCAAATTC	AGAACAATTGTT	TGTAATGT	PCCCCCTAC	TRATACCCC			217
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TrMDHcl :	:							- <u>:</u>	_
TrMDHc2	:					. <b></b>		:	_
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TrMDHc4 :	:					. <b> :</b>		- :	_
TrMDHc5 :	: '							- :	-
TrMDHc6:	:							- :	-
TrMDHc7 :	:							·- :	-
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TrMDHc17 :		TAAĢTAAATCTGCGAGA	AGCAGTTTATTG(	CTGCAGGGA	CTGAAATTA	AAACCAGTT	TTAGGTT	G:	380

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		*	1340	*	1360	*	1380		
TrMDHc1	:							- :	-
TrMDHc2	:							- :	-
TrMDHc3	:							- :	-
TrMDHc4	:							- :	-
TrMDHc5	:							- :	-
TrMDHc6	:							- :	-
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TrMDHc8	:							- :	-
TrMDHc9	:				-,			- :	-
TrMDHc10	:							- :	-
TrMDHcll	:							- :	_
TrMDHc12	:							- :	-
TrMDHc13	:							- :	_
TrMDHc14	:							- :	-
TrMDHc15	:							- :	-
TrMDHc16	:							- :	-
TrMDHc17	:	GCCTTTCCAT	TTCGTAATGGCCC	TCATTG	TTGCATGNTTTC	ATATAATGCA	ATTGAAGGGTG	<b>v</b> :	443
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		*	1400						
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TrMDHc2	:			: -					
TrMDHc3	:			: -					
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TrMDHc7	:			: -			•		
TrMDHc8	:			: -			•		
TrMDHc9	:			: -					

TrmDHd : GGGTAGGCGGAGATTTNAACCCATTTTCCTCTAAATCTCTCTCAACTTCTCTTTCCATT : 60 TrMDHd : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCAGCAGCAGCAGCTACTTTTACTA : 120 TrmDHd : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 180 TrMDHd : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240 TrMDHd : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTGCGTGCAACTTTTGCAC : 300 TrmDHd : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 360 TrmDHd : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420 TrMDHd : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480 TrMDHd : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540 TrmDHd : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAGAAA : 598

TrMDHd : MAASAAATFTIGTAQTGRPLPQSNPFGLKVNSQVNFKTFSGLKAMSSLRCESESSFFGNE : 60

100 TrMDHd : TSAALRATFAPKAQKENQNINRNLHPQASYKVAVLGAAGGIGQPLALLIKMSPLVSDLHL : 120

140 160

TrMDHd : YDIANVKGVAADISHCNTPSKVLDFTGASELANCLKGVDVVVIPAGVPR : 169

Figure 66 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHd

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		airam aga	aca ca muu					50	
TrMDHdl	:						MAACTTCTCTTTCCAT		60
TrMDHd2	:						C-ACTTCTCTTTCCA		58
TrMDHd3	:		GGAGATT	INAACCCA:I'I	TTCCTCTTAA	ATCTCTC	-CÄACTTCTCÄTTCCA1		52
			*	80	*	100	* 12	_	
TrMDHdl	:						PAGCAGCTACTTTTACT		120
TrMDHd2	:						CAGCAGCTACTTTTACT		118
TrMDHd3	:	CCCATTAC	CATTCAT	rcccaga@g1	;I;GAGATGGCA	GCATCAGO	CAGCAGCTACTTTTACT	ΙA :	112
			*	140	*	160	* 18		•
TrMDHdl	:						TTTTGGTTTGAAAGT		180
TrMDHd2							TTTTGGTTTGAAAGT		178
TrMDHd3	:	TTGGAACT	rgcccaaa	CAGGGAGGEC	CACTTCCTCAA	TCAAACCC	TTTTGGTTTGAAAGT	Α:	172
			1						
m-1077.77			*	200	*	220	* 24		
TrMDHd1							GTCATCTCTAAGATG		240
TrMDHd2							GTCATCTCTAAGATG		238
TrMDHd3	: 5	ATTCCCAG	•G'1"1'AA'1"1"	I"PAAGACCT'I	CTCTGGTCTC	AAGGCCA'I	CGTCGTCTCTAAGATG	(e :	232
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TrMDHd1 TrMDHd2							GCGTGCAACTTTTGC <i>I</i> GCGTGCAACTTTTGC <i>I</i>		300
TrMDHd2							.GCGTGCAACTTTTGCA .GCGTGCAACTTTTGCA		298
TIMDAGS		AGICIGA	ATCATCTT.	ICITIGGCAA	CGAAAC I IJG I	GCIGCICI	.GCGTGCAACTTTTGCA	(C :	292
				330		240	+ 3/	- ^	
T-MDUA1		~~» » » ~~	*	320	*	340	* 36	_	260
TrMDHd1				AAAACCAAAA		AATTTGCA	TCCTCAGGCATCCTA	Α:	360
TrMDHd2	:	CCAAAGCT	CAAAAGG	AAAACCAAAA AAAACCAAAA	CATCAACCGC	AATTTGCA AATTTGCA	ATCCTCAGGCATCCTAC	A :	358
	:	CCAAAGCT	CAAAAGG	AAAACCAAAA AAAACCAAAA	CATCAACCGC	AATTTGCA AATTTGCA	TCCTCAGGCATCCTA	A :	
TrMDHd2	:	CCAAAGCT	CAAAAGG	AAAACCAAAA AAAACCAAAA	CATCAACCGC	AATTTGCA AATTTGCA	ATCCTCAGGCATCCTAC	A :	358
TrMDHd2	:	CCAAAGCT	CAAAAGG	АААССАААА ААААССАААА АААЁООАААА	CATCAACCGC	AATTTGCA AATTTGCA AATTTGCA	ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ĞCCTCAGGCATCCTAC	CA: CA:	358
TrMDHd2 TrMDHd3	:	CCAAAGCT CCAAAGCT	CAAAAGGA CAAAAGGA	лаассааа лаассаааа лаассаааа лаассааа 380	CATCAACCGC CATCAACCGC	AATTTGCA AATTTGCA AATTTGCA 400	ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42	A : CA : CA :	358 352
TrMDHd2 TrMDHd3	:	CCAAAGCT CCAAAGCT	CCAAAAGGA CCAAAAGGA *	AAAACCAAAA AAAACCAAAA AAAACGAAA AAAACGAAA AAAACCAAAAAAAA	CATCAACCGC CATCAACCGC * AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT	ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42	CA: CA: CA:	358 352 420
TrMDHd2 TrMDHd3 TrMDHd1 TrMDHd2	:	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG	CAAAAGGA CAAAAGGA * * * * * * * * * * * * * * * *	AAAACCAAAA AAAACCAAAA AAAACCGAAA 380 GTGCTGCAGG	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42 AGCACTTCTCATTAAC	CA: CA: CA: CA:	358 352 420 418
TrMDHd2 TrMDHd3	:	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG	CAAAAGGA CAAAAGGA * * * * * * * * * * * * * * * *	AAAACCAAAA AAAACCAAAA AAAACCGAAA 380 GTGCTGCAGG	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT	ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42	CA: CA: CA: CA:	358 352 420
TrMDHd2 TrMDHd3 TrMDHd1 TrMDHd2	:	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG	CAAAAGGA CAAAAGGA * * * * * * * * * * * * * * * *	AAAACCAAAA AAAACCAAAA AAAACCGAAA 380 GTGCTGCAGG	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42 AGCACTTCTCATTAAC	CA: CA: CA: CA:	358 352 420 418
TrMDHd2 TrMDHd3 TrMDHd1 TrMDHd2	:	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG	CAAAAGGA CAAAAGGA * * * * * * * * * * * * * * * *	AAAACCAAAA AAAACCAAAA AAAACCGAAA 380 GTGCTGCAGG	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC * 42 AGCACTTCTCATTAAC	CA:	358 352 420 418
TrMDHd2 TrMDHd3 TrMDHd1 TrMDHd2	:	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG	CAAAAGGA CCAAAAGGA * * * * * * * * * * * * * * * *	AAACCAAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT CAGCCACT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC AGCCTCAGGCATCCTAC  * 42 AGCACTTCTCATTAAC AGCACTTCTCATTAAC AGCACTTCTCATTAAC	CA :	358 352 420 418
TrMDHd3 TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3	: :	CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG	CAAAAGGA CCAAAAGGA * * * * * * * * * * * * * * * *	AAACCAAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC  CATCAACCGC  * AGGAATTGGT AGGAATTGGT AGGAATTGGT AGGAATTGGT	AATTTGCA AATTTGCA AATTTGCA 400 CAGCCACT CAGCCACT CAGCCACT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCATTAAC AGCACTTCTCATTAAC AGCACTTCTCATTAAC ACCACTTCTCATTAAC ACCACTTCTCATTAAC ACCACTTCTCATTAAC ACCACTTCTCATTAAC ACCACTTCTCATTAAC ACCACTTCTCATTAAC	CA:	358 352 420 418 412
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3	: :	CCAAAGCT CCAAAGCT AAGTGGCCAAGTGGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CGTTCTTGG CGTTCTCGGG CTTGGTTTC	AAAACCAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC CATCAACCGC  * CAGCAATTGGT CAGGAATTGGT * CAGGAATTGGT * TCTTTATGAT TCTTTATGAT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT AGO ATCGCGAA	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCATTAAC ATCCACTTCACTTCACTTAAC ATCCACTTCACTTCACTTAAC ATCCACTTCACTTCACTTCACTTAACCACTT	CA :	358 352 420 418 412
TrMDHd1 TrMDHd2 TrMDHd2 TrMDHd3 TrMDHd3	: :	CCAAAGCT CCAAAGCT AAGTGGCCAAGTGGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CGTTCTTGG CGTTCTCGGG CTTGGTTTC	AAAACCAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC CATCAACCGC  * CAGCAATTGGT CAGGAATTGGT * CAGGAATTGGT * TCTTTATGAT TCTTTATGAT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT AGO ATCGCGAA	TCCTCAGGCATCCTAC TCCTCAGGCATCCTAC GCCTCAGGCATCCTAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC GCACTTCTCATTAAC TGCACTTCTCATTAAC  * 48 TGTTAAGGGAGTTGCT	CA :	358 352 420 418 412 480 478
TrMDHd1 TrMDHd2 TrMDHd2 TrMDHd3 TrMDHd3	: :	CCAAAGCT CCAAAGCT AAGTGGCCAAGTGGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CGTTCTTGG CGTTCTCGGG CTTGGTTTC	AAAACCAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC CATCAACCGC  * CAGCAATTGGT CAGGAATTGGT * CAGGAATTGGT * TCTTTATGAT TCTTTATGAT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT AGO ATCGCGAA	TCCTCAGGCATCCTAC TCCTCAGGCATCCTAC GCCTCAGGCATCCTAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC GCACTTCTCATTAAC TGCACTTCTCATTAAC  * 48 TGTTAAGGGAGTTGCT	CA :	358 352 420 418 412 480 478
TrMDHd1 TrMDHd2 TrMDHd2 TrMDHd3 TrMDHd3	: :	CCAAAGCT CCAAAGCT AAGTGGCCAAGTGGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CGTTCTTGG CGTTCTCGGG CTTGGTTTC	AAAACCAAAAAAAAACCGAAAAAAACCGAAAAAAAAAA	CATCAACCGC CATCAACCGC  * CAGCAATTGGT CAGGAATTGGT * CAGGAATTGGT * TCTTTATGAT TCTTTATGAT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT AGO ATCGCGAA	TCCTCAGGCATCCTAC TCCTCAGGCATCCTAC GCCTCAGGCATCCTAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC GCACTTCTCATTAAC TGCACTTCTCATTAAC  * 48 TGTTAAGGGAGTTGCT	CA :	358 352 420 418 412 480 478
TrMDHd1 TrMDHd2 TrMDHd2 TrMDHd3 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT	CAAAAGGA CCAAAAGGA * GGTTCTTGG GGTTCTĞGG * TTGGTTTGGTTTGGTTTGGTTTGGTTTGGTTTG	AAAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CATCAACCGC CATCAACCGC  * * * * * * * * * * * * * * * * *	AATTTGCA AATTTGCA 400 CAGCCACT CAGCCACT 460 ATCGCGAA ATCGCGAA ATCGCGAA	TCCTCAGGCATCCTAC TCCTCAGGCATCCTAC TCCTCAGGCATCCTAC  * 42 TGCACTTCTCATTAAC TGCACTTCTCATTAAC TGCACTTCTCATTAAC TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT	CA :	358 352 420 418 412 480 478
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3 TrMDHd3 TrMDHd1 TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CAAAAGGA CAAAAAGGA CATCTTGGTTTCC CTTGGTTTCC CTTGGTTTCC CAGTCATTC	AAAACCAAAA AAAACCAACACCAACAA	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTGCATTT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTACCT ATCCTCACTAAC ATCCTCACTAAC ATCCCACAGGTGCTTCTGAC ATCCCACAGGTGCTTCTGAC ACCCACAGGTGCTTCTGAC	TA :	358 352 420 418 412 480 478 472
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd1 TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CAAAAGGA CAAAAAGGA CATCTTGGTTTCC CTTGGTTTCC CTTGGTTTCC CAGTCATTC	AAAACCAAAA AAAACCAACACCAACAA	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTGCATTT	* 48 TGTTAAGGAGTTGCT  * 42 TGCACTTCTCATTAAC TGCACTTCTCATTAAC TGTTAAGGAGTTGCT TGTTAAGGAGTTGCT TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT	TA :	358 352 420 418 412 480 478 472
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd1 TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CAAAAGGA CAAAAAGGA CATCTTGGTTTCC CTTGGTTTCC CTTGGTTTCC CAGTCATTC	AAAACCAAAA AAAACCAACACCAACAA	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTGCATTT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTACCT ATCCTCACTAAC ATCCTCACTAAC ATCCCACAGGTGCTTCTGAC ATCCCACAGGTGCTTCTGAC ACCCACAGGTGCTTCTGAC	TA :	358 352 420 418 412 480 478 472 540 538
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd1 TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CAAAAGGA CAAAAAGGA CATCTTGGTTTCC CTTGGTTTCC CTTGGTTTCC CAGTCATTC	AAAACCAAAA AAAACCAAACACACCAACACCCAACACCCCAACACCCCCACCACCCC	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTGCATTT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTACCT ATCCTCACTAAC ATCCTCACTAAC ATCCCACAGGTGCTTCTGAC ATCCCACAGGTGCTTCTGAC ACCCACAGGTGCTTCTGAC	TA :	358 352 420 418 412 480 478 472 540 538
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCC AAGTGGCC TGTCGCCT TGTCGCCT TGTCGCCT CTGATATC	CAAAAGGACAAAAGGACAAAAGGACAAAAGGACATTCCCCCCCC	AAAACCAAAA AAAACCAACACCAACAA	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTGCATTT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTACCT ATCCTCACTAAC ATCCTCACTAAC ATCCCACAGGTGCTTCTGAC ATCCCACAGGTGCTTCTGAC ACCCACAGGTGCTTCTGAC	TA :	358 352 420 418 412 480 478 472 540 538
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd1		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGACAAAAGGACAAAAGGACAAAAGGACATTCCCCCCCC	AAAACCAAAA AAAACCAAAC GCAACCTGCA GCAACACTCC GCAACACTCC GCAACACTCC	CATCAACCGC CATCAACCGC  * AGGAATTGGT AGGAATTGGT TCTTTATGAT	AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT AGO ATCGCGAA ATTGCAA ATTGCAA TTGGATTT TTGGATTT	* 42 GGCACTTCTCATTAAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC GGCACTTCTCATTAAC TGCACTTCTCATTAAC TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT TGTTAAGGGAGTTGCT CACAGGTGCTTCTGAC CACAGGTGCTTCTGAC CACAGGTGCTTCTGAC	1	358 352 420 418 412 480 478 472 540 538 532
TrMDHd1 TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd1 TrMDHd2 TrMDHd3  TrMDHd2 TrMDHd3		CCAAAGCT CCAAAGCT AAGTGGCG AAGTGGCG AAGTGGCG TGTCGCCT TGTCGCCT TGTCGCCT TGTCGCCT TGTCGCCT TGTCGCCT	CAAAAGGA CAAAAGGA CAAAAGGA CAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAGGA CAAAAAAGAAAAAAAA	AAAACCAAAA AAAACCAACACCAACACCCAACACCCCAACACCCCCACAC	CATCAACGC CATCAACGC  A CATCAACGC  A CATCAACGC  A CATCAACGCT  A CATCAAACGTT  TTCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT  TTCAAAGGTT	AATTTGCA AATTTGCA AATTTGCA AATTTGCA AOO CAGCCACT CAGCCACT CAGCCACT ATTGCAA ATTGCAA ATTGCAA TTTGCATTT TTTGCATTT TTTGCATTT TTTGCATTT ATTGCATTT	TCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCAGGCATCCTAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTTAAC ATCCTCACTACCT ATCCTCACTAAC ATCCTCACTAAC ATCCCACAGGTGCTTCTGAC ATCCCACAGGTGCTTCTGAC ACCCACAGGTGCTTCTGAC	CA :	358 352 420 418 412 480 478 472 540 538 532

Figure 67 Consensus contig nucleotide sequence of TrMDHe

	•	*	20	*	40 ·	*	60	
TrMDHe :	TTNTNTTT	attitatgi	TTTTTNCCTCC	TACATATA	ACTCTTNACTTN	GCATACAC	rgtg :	60
						•		
		* .	80	*	100	* 	120 3466 :	120
TrMDHe :	TCTCTCAA	TTATTATT	AGTCCTTAGAAA	TGGAAGCA	CATGCAGCTGGA	GCCARICA	OACC .	
	٠					*	. 180	
m-MDTIc.	, , , , , , ,	* አአጥሮጥሮጥር፤	140 ~~~~~~~~~~	. * 'CTCCAAAT'	160 TTCCAGGAAGGA			180
TIMDHe:	ATTGCAAG	WHICTCIG	C1CH1C110.11					
		•	200	*	220	*	240	
TrMDHe :	ATTAGCAA	AGCTAACT(	GCAGAGCAAAAG		CCGGGATTCAA	AGTAGCAAT	CTTG :	240
		*	260	*	280	*	300	200
TrMDHe :	GGGGCTGC	TGGTGGAA'	TTGGTCAATCC	CTTTCTTTG	CTGTTGAAGAT	CAATCCATT	GGTT :	300
		*	320	*	340	* rcamammaG	360 TCAC :	360
TrMDHe :	TCAGTTCI	TCATCTTT	ATGATGTTGTC/	AACACTCCT	GGTGTCACTGC	IGHIGIIAC	TONG .	
					400	•	420	
m=MDUo	አመመረ፡አረ፡አር	* • ^ C	380 <b></b> TGGTTCGTGGC'	* rttctagge	400 CAGGCACAACT	rgagaatgo		420
IIMDRE :	AIIGACAC	.0010010	10011001100					
		*	440	*	460	*	480	
TrMDHe	: ACAGGCAT		TCGTTATACCT	GCTGGTGT	CCGAGGAAACC	TGGAATGAC	CAAGG:	480
		*	500	*	520	*	540	<b>540</b>
TrMDHe	GATGACT	ratttaaga	TAAATGCTGGA	ATTGTGAG	GACTCTTAGCGA	AGGAATTG	CCAAG :	540
		*	560	* ************************************	580 1202 CTG	* ሮልሮፕሮፕሮርር	600	600
TrMDHe	: AGCTGTC	CTAATGCAA	ATTGTCAACTTG	ATTAGCAA.	rccagtgaattc	CACIOIO		
					C40		660	
T-MDHA	• GCTGCTG	⋆ አርርጥጥጥፕሮ <i>፤</i>	620 AAGAAAGCCGGT	* 'ACATATGA'	640 TCCAAAGCGACT	TTTAGGGG'		660
TIMDITE	. 0010020							
	•	*	680	*	700	*	720	
TrMDHe	: ACCCTCG	ATGTTGTG!	AGGGCAAATACC	TTTGTGGC.	AGAAGTACTTGG	TGTTGATC	CAAGA :	720
		*	740	* .	760	*	780	=00
TrMDHe	: GAGGTTG	ATGTTCCA(	GTGGTAGGAGGG	CACGCAGG	AGTCACAATATI	ACCTCTTT	TGTCA :	780
								•
		*.	800	*	820 .	* "C" A C" A A NC"		840
TrMDHe .	: CAGGTTA	AGCCTCCC	AGTAGCTTCACC	CAGAAGA	AACCGAATACCT	. ORGENERALI		
					0.00		900	
ጥታለነገሁሉ	· CANANIC	* :GCGGDDCD	860 CAAGTTGTTGAC	* GCAAAGGC	880 TGGGGCTGGTT	 CGGCAACAC	TANTN :	900
TIMDRE	. CAMMING	CCCCARON						
		*	920	*	940	*	960	
TrMDHe	: ATGGCCT	TATGCAGCT	GCCAAGTTTGC	PAACGCATO	CCTCCGTGGCT	PGAAAGGAG	AAGCC:	960
			•					

\* 1040 \* 1060 \* 1080

TrMDHe : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG : 1080

\* 1100 \* 1120 \* 1140

TrmDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

\* 1160 \* 1180 **\*** 1200

TrmDHe : GTAGAATTCATCAAAAAAAAAAAAAAAAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 1200

\* 1220

TrMDHe : ATATCTATAAAGAACTTGTGTAATAATTCC : 1230

		* 20 * 40 * 60		
TrMDHe	:	MEAHAAGANQRIARISAHLQPPNFQEGGDVAISKANCRAKGGAPGFKVAILGAAGGIGQS	:	60
		* . 80 * 100 * 120		
TrMDHe	:	LSLLLKINPLVSVLHLYDVVNTPGVTADVSHIDTGAVVRGFLGQAQLENALTGMDLVVIP	:	120
		•		
		* 140 · * 160 * 180		
TrMDHe	:	AGVPRKPGMTRDDLFKINAGIVRTLSEGIAKSCPNAIVNLISNPVNSTVPIAAEVFKKAG	:	180
		•		
		* 200 * 220 * 240		
TrMDHe	:	TYDPKRLLGVTTLDVVRANTFVAEVLGVDPREVDVPVVGGHAGVTILPLLSQVKPPSSFT	:	240
		·		
		* 260 * 280 * 300		
TrMDHe	:	AEETEYLTXRIQXGGTQVVEAKAGAGSATLMAYAAAKFANACLRGLKGEAGIVECAFVDS	:	300
		* 320 * 340 . *		
TrMDHe				359
TIMDRE	•	QVTELPFFAAKVRLGRGGAEEIYQLGPLNEYERIGLEKAKKELAGSIQKGVEFIKKKXR :	-	103

Figure 69 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHe

		* 20 * 40 . * 60		
TrMDHe1		* 20 * 40 * 60 TINENTITATITATTTTATTTTTTTTTTTTTTTTTTTTTT		60
	•	TINENTITATITIATGITTITINCCTCCTACATATAACTCTTNACTINGCATACACTGTG	:	3
TrMDHe2	:	GTG	:	3
TrMDHe3	:		:	-
TrMDHe4	:		•	_
TrMDHe5	:		•	_
TrMDHe6	:		:	_
TrMDHe7	:		:	_
TrMDHe8	:		:	-
TrMDHe9	:		:	-
TrMDHe10	:	·	:	-
•		•		
		* 80 * 100 * 120		
TrMDHe1		TCTCT-AATTATTAGTCCTTCGAAATGGAAGCACATGCAGCTGCTACCAATCAGAGG	•	119
TrMDHe2	•	TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGTGCCAATCAGAGG		63
`TrMDHe3		TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGC@CATGCAGCTGGAGCCAATCAGAGG	:	63
TrMDHe4	•	GNAGTCCTTANAAATGGAAGCACATGCAGCTGGAGCCATCAGAGC	:	44
	•	GAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG	:	38
TrMDHe5	:	CENTGCAGCTGGAGCCAATCAGGG		26
TrMDHe6	:	- CEAN IGCAGC I GGI, GCCAN, I MNGAGG	•	26
TrMDHe7	:		:	_
TrMDHe8	:		•	_
TrMDHe9	:		•	_
TrMDHe10	:		:	-
		· * 140 * 160 * 180		
TrMDHe1		ATTGCAAGAATCTCTGCTCATCTTCAGCCTCCAAATTTCCAGGAAGGA	:	179
TrMDHe2		ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGA		123
TrMDHe3	:	ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGA	:	123
TrMDHe4	:	attgcaagaatctctgctcatcttc <mark>-</mark> gcctccaaatttccaggaaggaaggtgatgtgca	:	103
TrMDHe5	:	ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGA	:	98
TrMDHe6	:	ATTGC-AGAATCTCTGCTCATCTT-NACCTCC-AATTTCCAGGAAGGAGGTGATGTTGCA	:	83
TrMDHe7	•			· -
TrMDHe8	-		•	
			:	_
	:		:	-
TrMDHe9	:		:	- -
	:		:	- -
TrMDHe9	:		:	- -
TrMDHe9	:	* 200 * 220 * 240	:	:
TrMDHe9	: :	* 200 * 220 * 240 ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	:	239
TrMDHe9 TrMDHe10	: :		:	239
TrMDHe9 TrMDHe10 TrMDHe1	: : : : : : : : : : : : : : : : : : : :	ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG	: : : : : : : : : : : : : : : : : : : :	
TrMDHe9 TrMDHe10 TrMDHe1 TrMDHe2		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGC <u>E</u> AAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183
TrMDHe9 TrMDHe10 TrMDHe1 TrMDHe2 TrMDHe3	• • • • • • • • • • • • • • • • • • • •	ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183
TrMDHe10  TrMDHe1 TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe4 TrMDHe5		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183 163
TrMDHe10  TrMDHe1 TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe5		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183 163 158
TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe5 TrMDHe6		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183 163 158
TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe6 TrMDHe7 TrMDHe8		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCÄAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183 163 158
TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe5 TrMDHe6		ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCÄAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG		183 183 163 158

		* 260 * 280 * 300		
TrMDHe1		* 260 * 280 * 300 GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT		
TrMDHe2	:	GGGGCTGCTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	:	299
TrMDHe3		GGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	•	
TrMDHe4	:	GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	:	
TrMDHe5	:	GGGGCTGCTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	:	223
TrMDHe6	·	GGGGCTGCTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT	:	218 203
TrMDHe7			:	203
TrMDHe8			:	-
TrMDHe9			•	-
TrMDHe10	:		•	-
	•		:	-
•				
		* 320 * 340 * 360		
TrMDHel	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC		359
TrMDHe2	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	:	303
TrMDHe3	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	:	303
TrMDHe4	:	TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	•	283
TrMDHe5	:	TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	•	203 278
TrMDHe6	:	TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC	:	278 263
TrMDHe7	:	THE TOTAL CONTROL OF THE TOTAL		203
TrMDHe8	:		:	<del>-</del> -
TrMDHe9	:		•	<del>-</del>
TrMDHe10	:			<u>-</u>
	•	,	•	-
		* 380 . * 400 * 420		
TrMDHe1	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	:	419
TrMDHe2	:	ATTGACACCGGTGCTGGTTCGTGGCTTTCTAGGGCAGGCA	:	363
TrMDHe3	:	ATTGAÏACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT	:	363
TrMDHe4	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	•	343
TrMDHe5	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA	ļ	338
TrMDHe6	:	ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCA		323
TrMDHe7	:			22
TrMDHe8	:			_
TrMDHe9	:		:	_
TrMDHe10	:		:	_
TrMDHe1		* 440 * 460 * 480		
	•	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	479
TrMDHe2 TrMDHe3	:	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	423
TrMDHe4	•	ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG		
TTIMBET		A CA COCA ELCCA COMPACTOR CONTRACTOR CONTRAC	:	423
TYMDUAE	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403
TrMDHe5	:	ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG		403 398
TrMDHe6	:	ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG		403 398 383
TrMDHe6 TrMDHe7	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGGTGTGCCCGAGGAAACCTGGAATGACAAGG		403 398
TrMDHe6 TrMDHe7 TrMDHe8	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403 398 383
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGÄTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403 398 383
TrMDHe6 TrMDHe7 TrMDHe8	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403 398 383
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9	:	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGÄTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG	:	403 398 383
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9	: : : : : : : : : : : : : : : : : : : :	ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540	:	403 398 383
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9	: : : : : : : : : : : : : : : : : : : :	ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540	: : : : : : : : : : : : : : : : : : : :	403 398 383 82 - -
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10	: : : : : : : : : : : : : : : : : : : :	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	: : : :	403 398 383 82 - - -
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10	: : : : : : : : : : : : : : : : : : : :	ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG	: : : : : : : : : : : : : : : : : : : :	403 398 383 82 - - - 539 483
TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10 TrMDHe1	: : : : : : : : : : : : : : : : : : : :	ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTCTGAAGGAATTGCCAAG	: : : : :	403 398 383 82 - - - 539 483 483
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTGAAGGAATTGTCAAG	: : : : : : : : : : : : : : : : : : : :	403 398 383 82 - - - 539 483 483 463
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTGAAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTGAAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTTGAAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTTGAAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTTGAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTTT		403 398 383 82 - - - 539 483 483 463 458
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGICAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGCCAAG		403 398 383 82 - - - - 539 483 463 458 443
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGÄTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGÄTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTÄCÄGAAGGAATTGÄCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTÄCÄGAAGGAATTGÄCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTÄCÄGAAGGAATTGÄCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTÄCÄGAAGGAATTGÄCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTÄCÄGAAGGAATTGÄCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		403 398 383 82 - - - 539 483 483 463 458
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe6		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540 GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTAAGGATAAATGCTAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTTTTAAGAATAAATGCTAAAATGCTAAGATTGTCAAGGACTCTTTTTTTAAGATAAATGCTAAAATTGTTAAGATTATTTAAGATAAATGCTAAATTGTAAGAATTGTTAAGAATAGATAAATGCTAAAATTGTTAAGAATTGTAAGAATTGTAAGAATTGTAAAATGCTAAGAATTGTAAGAAATGCTAAAATGCTAAGAATTGTAAGAAATGCTAAAATGCTAAAATGCTAAGAATTGTAAGAAATTGTAAAAATGCTAAAATTGTAAGAAATTGTAAAAATGCTAAAGAATTGTAAAAATGCTAAAATTGTAAAAATGCTAAAGAATTATTAAGAAAATGCTAAAATTGTAAGAAATTGTAAGAAATTGTAAAAATGCTAAAAATTGTAAAAATTGTAAAGAATTAAAATTGCCAAAGAATTTATAAGAATAAATGCTAAAATTGTAAAGAATTATTAAAGAAATTGCCAAAGAATTTAAAGAATAAATTGCCAAAGAATTTAAAGAATAAATTGCCAAAGAATTTAAAGAATAAATTGCTAAAATTGTAAAATTGTAAAATTGTAAAAATTGCTAAAGAATTAAAATTGCCAAAGAATTTAAAAATTGCCAAAGAATTTAAAAATTGCCAAAGAATTTAAAAATTAAAAATTGCTAAAATTAAAATTGTAAAATTGTAAAAATTGCTAAAAATTGCCAAAGAATTTAAAAAATTAAAATTGCTAAAATTGTAAAATTGTAAAAATTGCTAAAAATTGCCAAAGAATTTATTAAAGAAAAATTGCCAAAGAATTTATTAAAGAAAATTAAAATTGCTAAAATTGTAAAATTGTAAAAATTAAAAATTAAAAATTAAAATTAAAATTATT		403 398 383 82 - - - - 539 483 463 458 443
TrMDHe6 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe6 TrMDHe7 TrMDHe8		ACAGGCATGGACTTGGECGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG  * 500 * 520 * 540  GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		403 398 383 82 - - - - 539 483 463 458 443

	* 560 * 580 * 600	
TrMDHe1 :	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT	: 599
TrMDHe1 :	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT	: 543
TrMDHe3 :		: 543
TrMDHe4 :	AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT	: 523
		: 518
TrMDHe5 :		: 503
TrMDHe6 :		: 202
	AGCIGICCIAMIGCAMITGICAMCTIGNITACCAMICS	
TrMDHe8 :		: -
TrMDHe9		· -
TrMDHe10		•
	* 620 * 640 * 660	
TrMDHe1	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTANGGGGTAACA	: 659
TrMDHe2	GCTGCTGAGGTTTTCAAGAAAGCCGGTACAT	: 574
TrMDHe3	GCTGCTGAGGTCTTCAAGAAAGCCGGTACATAT	: 576
TrMDHe4	CCTCCTCDCCTCTCDAGDAGCCCGTDCATATGATCCAAAACGACTTTTAGGAGTTACA	: 583
TrMDHe5	GCTGGTGAGGTGTTCAAGAAGCCGGNACATATGATCCAAAACNACTTTTANGGGGTTACA	: 578
TrMDHe6	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAG	: 555
TrMDHe7	GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATECAAAGCGACTTTTAGGGGTAACA	: 262
TrMDHe8	TATGATCC-ACGCGACTTTTAGG-GGTACA	: 28
TrMDHe9		: -
TrMDHe10		: -
	* 680 * 700 * 720	<i>c</i> n2
TrMDHe1	: ACCCTCGATGNTGT	: 673
TrMDHe2	:	: -
TrMDHe3	:	. 503
TrMDHe4	: ACCCTCGATG	: 593
TrMDHe5	: ACCCTÑGATGTTGÌNGAGGGCAAATACI¦TTTGTGGCANAAG-NCTTGGNGTTGANCCCANA	: 637
TrMDHe6	:	: 322
TrMDHe7	ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA	: 322
TrMDHe8	: ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA	: 00
TrMDHe9	;	
TrMDHe10	:	
		•
		•
	* 740 * 760 * 780	•
TrMDHe1	* 740 * 760 * 780 :	· : -
TrMDHe1 TrMDHe2	* 740 * 760 * 780 :	: - : -
	* 740 * 760 * 780 :	: - : - : -
TrMDHe2	;	: -
TrMDHe2 TrMDHe3	* 740 * 760 * 780  :	: - : - : - : - : 693
TrMDHe2 TrMDHe3 TrMDHe4	NAGGGTNATNTTCCANTGGTAGGAGGGCCCCNGGANT-ACAANATTACC-CTTTTNT-	: -
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5	: NAGGETNATNTTCCANTGGTAGGAGGCCCCCNGGANT-ACAANATTACC-CTTTTIT: GAGGTTGATGTTCCAGNGGTAGGAIGGCACGCANGAGT-ACAATATTACCTCTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6	NAGGGTNATNTTCCANTGGTAGGAGGGCGCCCNGGANT-ACAANATTACC-CTTTTITT-	: -
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7	: WAGGGTWATWITCCAWIGGTAGGAGGCCCCCGGAWIT-ACAAWATTACC-CTTTIUT- : GAGGTTGATGTTCCAGMGGTAGGAMGGCACGCAMGAGT-ACAATATTACCTCTTTTGTCA : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8	: NAGGETNATNTTCCANTGGTAGGAGGCCCCCNGGANT-ACAANATTACC-CTTTTIT: GAGGTTGATGTTCCAGNGGTAGGAIGGCACGCANGAGT-ACAATATTACCTCTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe8	: WAGGGTWATWITCCAWIGGTAGGAGGCCCCCGGAWIT-ACAAWATTACC-CTTTIUT- : GAGGTTGATGTTCCAGMGGTAGGAMGGCACGCAMGAGT-ACAATATTACCTCTTTTGTCA : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe8	: NAGGGTNATNTTCCANTGGTAGGAGGCCCCNGGANT-ACAANATTACC-CTTTTNTGAGGTTGATGTTCCAGNGGTAGGANGGCACGCANGAGT-ACAATATTACCTCTTTTGTCAGAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTGTCAGAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe8 TrMDHe9	: NAGGGTNATNTTCCANTGGTAGGAGGGCGCGCNGGANT-ACAANATTACC-CTTTTNT : GAGGTTGATGTTCCAGNGGTAGGANGGCCACGCANGAGT-ACAATATTACCTCTTTTGTCA : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10	: NAGGGTNATNTTCCANTGGTAGGAGGCCCCNGGANT-ACAANATTACC-CTTTTNTGAGGTTGATGTTCCAGNGGTAGGANGGCACGCANGAGT-ACAATATTACCTCTTTTGTCAGAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTGTCAGAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTTGTCA	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10	# 800 * 820 * 840	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10 TrMDHe1 TrMDHe1 TrMDHe2 TrMDHe3	# 800 * 820 * 840	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10 TrMDHe1 TrMDHe1 TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe3 TrMDHe4	# 800 * 820 * 840	: - : 381
TrMDHe2 TrMDHe3 TrMDHe4 TrMDHe5 TrMDHe6 TrMDHe7 TrMDHe8 TrMDHe9 TrMDHe10  TrMDHe1 TrMDHe1 TrMDHe2 TrMDHe3 TrMDHe3 TrMDHe4 TrMDHe4 TrMDHe5	# 800 * 820 * 840	: - : 381
TrmDHe2 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe7 TrmDHe8 TrmDHe9 TrmDHe10  TrmDHe1 TrmDHe1 TrmDHe2 TrmDHe2 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6	MAGGETMATMTTCCAMTGGTAGGAGGCCCCCMGGAMT—ACAAMATTACC—CTTTTMT— GAGGTTGATGTTCCAGMGGTAGGAMGGCACGCAMGAGT—ACAATATTACCTCTTTTGTCA GAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTGTCA  * 800	: - : 381
TrmDHe2 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe8 TrmDHe9 TrmDHe10  TrmDHe1 TrmDHe1 TrmDHe2 TrmDHe3 TrmDHe3 TrmDHe4 TrmDHe6 TrmDHe6 TrmDHe7	MAGGETMATMTTCCAMTGGTAGGAGGCCCCCMGGAMT—ACAAMATTACC—CTTTTMT— GAGGTTGATGTTCCAGMGGTAGGAMGGCACGCAMGAGT—ACAATATTACCTCTTTTGTCA GAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTGTCA  * 800	: - : 381 : 148 : - : -
TrmDHe2 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe7 TrmDHe8 TrmDHe9 TrmDHe10  TrmDHe1 TrmDHe2 TrmDHe2 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe7 TrmDHe6 TrmDHe7 TrmDHe8	# 800 * 820 * 840	: - : 381 : 148 : - : -
TrmDHe2 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe7 TrmDHe8 TrmDHe9 TrmDHe10  TrmDHe1 TrmDHe1 TrmDHe2 TrmDHe3 TrmDHe3 TrmDHe4 TrmDHe5 TrmDHe6 TrmDHe6	MAGGETMATMTTCCAMTGGTAGGAGGCCCCCMGGAMT—ACAAMATTACC—CTTTTMT— GAGGTTGATGTTCCAGMGGTAGGAMGGCACGCAMGAGT—ACAATATTACCTCTTTTGTCA GAGGTTGATGTTCCAGTGGTAGGAGGCCACGCAGGAGTCACAATATTACCTCTTTTGTCA  * 800	: - : 381 : 148 : - : - : - : - : - : - : - : -

M. sames	*	860	*	880	* 9	00
TrMDHel	:					: -
TrMDHe2	:					: -
TrMDHe3	:					
TrMDHe4	:					·
TrMDHe5	:					: -
TrMDHe6	:					: -
TrMDHe7	: CAAAANGGCGGAACA					: -
TrMDHe8	CARAMIOGEGGAACA	CAAGIEGIIGAG	SCAAAG			: 473
TrMDHe9	: CAAAATGGTGGAACA	SAAGTTGTTGAG	GCAAAGGC'	regeecteettee	GCAACACTAN	IA : 268
	:	GITTGTTGAG	GCAAAGGC'I	rggggctggttce	GCAACACTAN	IN: 42
TrMDHe10	:	TTGTTGAG	GŅAAAGGC	RGGGGCTGGTTCG	G-NAC-CT-N	IN : 38
						-74
	*	920	*	940	* 9	60
TrMDHe1						
TrMDHe2	:					: -
TrMDHe3	:					• -
TrMDHe4	:					
TrMDHe5	:					: -
TrMDHe6						: -
TrMDHe7						: -
TrMDHe8	ATCCCMTATCCACCT					: -
TrMDHe9	ATGGCATATGCAGCTC	JCCAAGTTTGCTA	ACGCATGC	CTCCGTGGCTTG	AAAGGAGAAG	C: 328
TrMDHe10	: ATGGCCTATGCAGCTC	CCAAGTTTGCTA	ACGCATGC	CTCCGTGGCTTG	AAAGGAGAAG	C: 102
immero	: ATGGCCTATGCAGCTC	CC-AGTTTGCTA	ACGCATGC	CTCCGTGGCTTG	AAAGGAGAAG	C: 97
						_
	*	980	*	1000	* 102	20
TrMDHe1						
TrMDHe2	:					: _
TrMDHe3	:					
TrMDHe4	:					-
TrMDHe5	:	•				- : -
TrMDHe6						- : -
TrMDHe7	:					-: -
TrMDHe8	: GGGATAGTGGAGTGTG	CTTTTTTCTTCTTCTTT	emer cem			-
TrMDHe9	: GGGATAGTGGAGTGTG	CITITGITGATT	CTCAGGTT	ACGGAACTTCCT	TTCTTTGCAGC	C : 388
TrMDHe10	. POLICE COMOTOTO	CTTTTGTTGATT	CTCAGGTT	ACGGAACTTCCT	TCTTTGCAGC	C : 162
	: GGGATAGTGGAGTGTG	CITIGITGATT	CTCAGGTT.	ACGGAACT"TCCT"	TTCTTTGCAGC	<b>E</b> : 157
	*	1040		1060	+ 100	•
TrMDHe1	:	1010			* 108	O
TrMDHe2			<b></b>			- : -
TrMDHe3	•					- : -
TrMDHe4						- ; -
TrMDHe5	,					-: -
TrMDHe6	,					- : -
TrMDHe7						- : -
						- : -
TrMDHe8	AAGGTTCGTCTTGGTC	GCGGTGGAGCAG	AAGAGATA	fa <mark>gcaacttggt</mark> c	CCCTTAATGA	<b>E</b> : 448
TrMDHe9	HAGGIICGICIIIGGIC	GCGGTGGAGCAG	AAGAGATAT	ΓΑΤΟΆΑΟΤΤΟΩΤΟ	יר כי כי תידים אידים אי	A
TrMDHe10	AAGGTTCGTCTTGGTC	GCGGTGGAGCAG	AAGAGATAT	PATCAACTTGGTC	CCCTTAATGA	6 : 217
	•					
	*	1100	* 1	1120	* 114	0
TrMDHel						- · -
TrMDHe2			- <b></b>			
TrMDHe3						•
TrMDHe4						•
TrMDHe5						- : -
TrMDHe6						- : -
TrMDHe7						- : -
TrMDHe8	TATGACACCAGO	ricio a a a a a				-
TrMDHe9	TATGAGAGGATTGGGTT	I GGAAAAAGCGAA	GAAUGAGI	TAGCGGGAAGCA	TCCAGAAGGG	: 508
TrMDHe10	TATGAGAGGATTGGATT	AGAAAAAGCGAA	AGAAAGAGT	'TAGCAGGAAGCA'	TCCAGAAGGG	: 282
	TATGAGAGGATTGGATT	.AGAAAAAGCGAA	GAAAGAGI	'TAGCAGGAAGCA'	TCCAGAAGGG	: 277

			*	1160	*	1180	*-	1200		
TrMDHe1	:								:	-
TrMDHe2	:				-,				:	-
TrMDHe3	:								:	-
TrMDHe4	:								:	-
TrMDHe5	:								:	-
TrMDHe6	:								:	-
TrMDHe7	:								:	
TrMDHe8	:	GTAGAATT	CATCAGA	AAAUAAGEGAGAT	AAGG	AAAAATTAGT'	TTTGTATTGNC:	CTITICI	:	568
TrMDHe9	:			NAAAAANAA					:	306
TrMDHe10	:	GTAGAATT	CATCAAA	AAAAAN	- <i></i> -	<del>-</del>			:	299
			*	1220	*	·				
TrMDHe1	:				:	-				
TrMDHe2	:				:	-	•			
TrMDHe3	:				:	-				
TrMDHe4	:				:	-				
TrMDHe5	:				:	-				
TrMDHe6	:				:	_				
TrMDHe7	:				:	Α				
TrMDHe8	:	ATATCTAT.	AAAGAAC	TTGTGTAATAATI	CC :	598				
TrMDHe9	:				:	-				
TrMDHe10	:				:	-				

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		*	20	*	40	*	60		
TrMDHf	:	GNNTACNGCTATCNAC	CCTTCTTTCTTA:	PACAATAA?	inatagata <u>a</u> at	TCATCTGCT	AAA	:	60
							120		
		*	80	*	100	** ***********************************	120		120
TrMDHf	:	TTATGGAGCCAAATTC	AGATGCAAATCA	ACGAATCG	CAAGAATCTCCG	GCCACCTA	WIC	•	120
						•			
			140	*	160	*	180		
TrMDHf		CTCCCAATTTCAAGAT		ተር <b>ል</b> ሞተርጥጥ		TCCATTGC		:	180
TIMONI	٠	CICCCMIIICMONI	OMITOMICAL CO.	10.111011					
				•					
	•	*	200	*	220	*	240		
TrMDHf	:	CAAAAGGTGGAGCACC	TGGATTCAAAGT	TGCAATTT'	TAGGTGCTGCT	GTGGCATA	GTC	:	240
									•
•					•				
		*	260	*	280	*	300		200
TrMDHf	:	AACCTCTTTCAATGTT	'GATGAAGATGAA'	TCCTTTGG	TTTNAGTTCTTC	ATCTTAT	JATG	:	300
		*	320	*	340	*	360		
TrMDHf		TTGTTAATACTCCTGG		TATTAGTC		CTGCTGTT		:	360
	•								
				·					
		*	380	*	400	*	420		
TrMDHf	:	GAGGGTTTTTGGGGCA	AAATCAGCTTGA	GGATGCAC	TTACAGGTATGO	BATTTGGTA	ATCA	:	420
		•			460	•	480		
mVmtt.£		TTCCTGCCGGTGTTCC	440	አ አማርማርአ	460 aaaamaamama	מידע מידע מידערן			480
TrMDHf	:	TTCCTGCCGGTGTTCC	CCGIAAACCIGG	ANIGACAA	GAGAIGAICIC.	LICHALMIN		•	
		*	500	*	520	*	540		
TrMDHf	:	CCGGGATCGTTAAAAC	CACTCTGTGAAGC	AATTGCAA	AGCGATGTCCT?	AGGCGATT	GTCA	:	540
					•				
		*	560	*	580		600		600
TrMDHf	:	ACGTGATTAGTAATCO	CGGTTAACTCCAC	TGTCCCCA	TTGCGGCTGAAC	TTTTCAAA.	HGMG	•	800
		*	620	*	640	*	660		
TrMDHf	:	CCGGTACTTATGATCC		GGGAGTGA	CAATGCTTGAT	STGGTTCGG	GCCA	:	660
		*	680	*	700 ·	*	720		
TrMDHf	:	ATACGTTTGTGGCTG	AGTTCTTGGTCT	TGATCCAA	GGGATGTGGAT	STCCCAGTT	G.T.C.G	:	720
		•	740	*	760	*	780		
TYMDHE		GAGGACATGCCGGAAT		TCTGCTTT		CACATTCC		:	780
	•				<del></del>		_		
		•							
		*	800	*	820	*	840		
$\mathtt{TrMDHf}$	:	TCACGACAAAGGAAAT	TGAGTACTTGAC	AGATCGCA	TACAAAACGGT	GAACTGAA	GTTG	:	840
			0.60						
		*	860						

TrMDHf : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866.

TrmDHf : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ : 60 TrmDhf : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120 TrmDHf : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180  ${\tt TrMDHf} \; : \; {\tt GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF} \; : \; 240$ 

TrMDHf : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268

Figure 72 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHf

TrMDHf1 TrMDHf2 TrMDHf3	:	* 20 * 40 * 60 GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA	:	60 - -
TrMDHf1 TrMDHf2 TrMDHf3	:	* 80 * 100 * 120 TTATGGAGCCAAATCAGATGCAAATCACGAATCGCAAGAATCTCCGGCCACCTAAATC	:	120 - -
TrMDHf1 TrMDHf2 TrMDHf3	:	* 140 . * 160 * 180 CTCCCAATTTCAAGATGAACATGGTGATTCTTTTGACAAGTTTCCATTGCCGTG	: :	180 - -
TrMDHf1 TrMDHf2 TrMDHf3	:	. * 200 * 220 * 240 CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGGTGGCATAGGTÜ	:	240 12 -
TrMDHf1 TrMDHf2 TrMDHf3	:	* 260 * 280 * 300  AACCTCTTTCAATGTTGATGAAGATGAATCCCTTGGTTT-AGTTCTTCATCTTTATGATG ACCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCTTTATGATG	: :	299 70 29
TrMDHf1 TrMDHf2 TrMDHf3	:	* 320 * 340 * 360  TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCACATGGATACTGGTGCTGTTGTTC  TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC  TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTC	:	359 130 86
TrMDHf1 TrMDHf2 TrMDHf3	: : :	* 380 * 400 * 420 GAGGATTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA	: :	419 190 146
TrMDHf1 TrMDHf2 TrMDHf3	:	* 440 * 460 * 480  TTCCTGCIEGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG  TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG  TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG	:	479 250 206
	:	* 500 * 520 * 540  CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCGAAGCGATGTCCTAAGGCGATTGTCA  CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA  CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGGTTGTCA		539 310 266
TrMDHf1 TrMDHf2 TrMDHf3	:	* 560 * 580 * 600  ACGTGATTAGTAATCCGGTTAACTCCACTGTCC  ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG	:	572 370 326

TrMDHf1	:		*	620	*	640	*	660	
TrMDHf2	:	CCGGTACT	TATGATCC	CAAGAGACTTTT	GGGAGTGA	CAATCCTTCATC	Teerree	2007	430
TrMDHf3	:	CCGGTACT	TATGATCO	CAAGAGACTTTT	GGGAGTGA	OTADITODIADI OTADITODIAGO	TGGTTCGG	GCCA:	386
					000.1010.	.c.ii.i.oci rofiic	10011000	SCCE .	300
TrMDHf1			*	680	*	700	*	720	
TrMDHf2		ATACCTO		Acumomecaman				:	-
TrMDHf3	:	ATACGITI	GIGGCIGA TTCCCTCA	AGTTCTTGGTCT	TGATCCAA	GGGATGTGGATG	TCCCAGTT	erree :	490
TEMBLES	•	MIACGILI	3100C1GA	AGTTCTTGGTCT	IGAT CCAA	GGGATGTGGATG	TCCCAGTT	errece :	446
			*	740	*	760	*	780	
TrMDHf1	:							:	_
TrMDH£2	:	GAGGACAT	GCCGGAAT	CACCATTTTACC'	TCTGCTTT	CTCAGGTTAAAC	CACATTCC	CTT :	550
TrMDHf3	:	GAGGACAT	ECCGGAAT	CACCATTTTACC	TCTGCTTT	CTCAGGTTAAAC	CACATTCC	rctt :	506
			*	800	*	820	•	840	
TrMDHf1	:							040	_
TrMDHf2	:	TCACGACA	AGGAAAT	TGAGTACTTG					576
TrMDHf3	:			TGAGTACTTGAC	AGATCGCA	TACAAAACGGTG	GAACTGAAC	TTG:	566
									300
			*	860					
TrMDHfl	:				-				
TrMDHf2	:			:	-				
TrMDHf3	:	TTGAGGCC <i>X</i>	AAGCTGG.	AGCTGGCTCT :	592				

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		* 20 * 40 * 60		
TrMDhg	:	GTAGGCAGCATCTAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAA	:	60
Mark Dir.		* 80 * 100 * 120		
Trmbng	:	TACGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTTT	:	120
		* 140 * 160 * 180		
TrMDhg	:	TAGATACATGTGTGTCTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGG	:	180
		* 200 * 220 * 240		
TrMDhg	:	TGCTGCAGGACAAATTGGNTATGCTCTTGNTCCAATGATTGCAAGAGGGATGATGCTAGG	:	240
		* 260 * 280 .* 300		
TrMDhg	:	CCCAAATCAACCTGGAATTCTTCATATGCTNGATATTGAACCAGGATTAGAGGCCCTTAA	:	300
	•	* 320 * 340 * 360		
TrMDhg	:	AGGGGTGAAGATGGATGATGATGGTGCTTCCCACTTCTTAGAGGTGTTGTTGCTAC	:	360
		* 380 * 400 * 420		
TrMDhg	:	TACGGATGTTGATGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCC	:	420
		* 440 * 460 * 480		
TrMDhg	:	AAGGAAGGAATGGAAAGAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGC	:	480
		* 500 * 520 * 540		
TrMDhg	:	TCAAGCTTCAGCTTTGGAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAA	:	540
		* 560 * 580 *		
TrMDhg	:	TCCAGCAAACACAAATGCTCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA :	5	99

## rigure 74 Deduced amino acid sequence of TrMDHg

TrMDhg : MCGLLKVDKEPVTVLVTGAAGQIXYALXPMIARGMMLGPNQPGILHMXDIEPGLEALKGV : 60

TrMDhg : KMELIDGAFPLLRGVVATTDVVEACKDVNIAVMLGGSPRKEGMERKDVMSKNVSIYKAQA : 120

TrMDhg : SALEEHAAADCKVLVVANPANTNALILKEFAPSIPEK : 157

Figure 75 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHg

TrMDHg1 TrMDHg2	ONDIGO A MORRA A CAR CHARLES AND A CAR CHARLES A	7
TrMDHg1 TrMDHg2	* 80 * 100 * 120  : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTTT	
TrMDHg1 TrMDHg2	* 140 * 160 * 180  : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 18 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 18	4
TrMDHg1 TrMDHg2	* 200 * 220 * 240  AGGACAAATTGGNTATGCTCTTGNTNCAATGATTGCNANAGGGATGATGCTANGNCCAAATC : 24  AGGACAAATTGGTTATGCTCTTGTTCCAATGATTGCAAGAGGGATGATGCTAGGCCCAAATC : 24	6 3
TrMDHg1 :	* 260 * 280 * 300 * 270	5 5
TrMDHg1 :	320 , * 340 * 360 * ATGGAACTGATTGATGGTGCTTCCCACTTCTTAGAGGTGTTGTTGCTACTACGGATGTTGT : 36	- 7
TrMDHg1 :	380 * 400 * 420 *  TGAAGCATGCAAGGATGTTAACATTGCTTGTTGTTGGTGGATCCCCAAGGAAGG	-
TrMDHgl : TrMDHg2 :	440 * 460 * 480 *  TGGAAAGAAAGATGTTAAGAATGTTTCAATTTACAAGGCTCAAGCTTCAGCTTTG : 491	•
TrMDHg1 : TrMDHg2 :	500 * 520 * 540 * 5  GAGGAGCATGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAATCCAGCAAACACAAATGC : 553	
TrMDHg1 : TrMDHg2 :	580 * TCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 594	

TrmDHh : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA : TrmDHh : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120 TrmDHh : CTCCCAATTTCAAGATGAACATGGTGATTCTTTTTGACAAGTTTCCATTGCCGTG : 180 TrmDHh : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGGTGGTGGCATAGGTC : 240 TrmDHh : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTTNAGTTCTTCATCTTTATGATG : 300 TrMDHh : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 360 TrMDHh : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420 TrmDHh : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480 TrMDHh : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540 TrmDHh : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 600 TrmDHh : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660 Trmdhh : Atacgtttgtggctgaagttcttggtcttgatccaagggatgtggatgtccagttgtcg : 720 TrmDHh : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 780 TrMDHh : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 840

\* 860

TrMDHh : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866

TrMDHh : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268

TrMDHh	:	* 20 * 40 * 60 MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ	:	60
TrMDHh	:	* 80 * 100 * 120 PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII	:	120
TrMDHh	:	* 140 * 160 * 180 PAGVPRKPGMTRDDLFNINAGIVKTLCEÄIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA	:	180
TrMDHh	:	* 200 * 220 * 240 GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF	:	240
		* 260		

Figure 78 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHh

		*	20	*	40	* 60	
TrMDHh1 :		GNNTACNGCTATCNA	ACCCTTCTTTC'	TATACAAT	AATNATAGATA	AATTCATCTGCTAAA	: 60
TrMDHh2 :							· •
TrMDHh3 :	:						
		*	80	*	100	* 120	
TrMDHh1		TTATGGAGCCAAAT'	rcagatgcaaa	TCAACGAAT	CGCAAGAATCT	CCGGCCACCTAAAT	: 120
TrMDHh2	:						- : -
TrMDHh3	:						, i
		*	140	*	160	* 18	
TrMDHh1	:	CTCCCAATTTCAAG	ATGAATGAACA	TGGTGATT	CTTCTTTGACA	AGTTTCCATTGCCGT	e : 180
TrMDHh2	:						- : -
TrMDHh3	:						
		*	200	*	220	* 24	
TrMDHhl	:	CAAAAGGTGGAGCA	CCTGGATTCAP	AGTTGCAA	TTTTAGGTGCT	GCTGGTGGCATAGGT GTGNCATAGGT	E : 240
TrMDHh2	:					GIGNCAIMGGI	- : -
TrMDHh3	:						
		*	260	*	280	* 30	
TrMDHhl	:	AACCTCTTTCAATG	TTGATGAAGA'	TGAATCCCT	TGGTTT-AGTT	CTTCATCTTTATGAT	G : 233
TrMDHh2	:	ACCCTCTTT-NATO	TTGATGAAGA'	ING/AVAVICE I	TGGTTTPAGTT	CTTCATCTTTATGAT CTTATNCTTTATGAT	G : 29
TrMDHh3	:						
		*	320	*	340	* 3 (	
TrMDHh1	:	THE RESERVE THE PROPERTY OF THE PARTY OF THE	na amamma amm		KANKATA KIJA L	ACTGGTGCTGTTGT	
TrMDHh2 TrMDHh3	:	TTGTTAATACTCC	rggrg-TACTT	CTGATATTA	GT-ATATGGAT	ACTGCTGCTGTTGT	r <b>c</b> : 86
1111011113	•	110 1					
					400	* 4:	20
		*	380	TTGAGGAT	400	ATGGATTTGGTAAT	CA : 419
TrMDHh1 TrMDHh2	:	ON COOPERFEE TO COO	<b>っこみ み み み ず ぐ み ら ぐ</b>	TITGAGGAT	CACTTACAGG	MIGGALITOGIVALE	31.
TrMDHh3	:	GAGGGTTTTTGGG	GCAAAATCAGC	TTGAGGAT	GCACTTACAGGT	PATGGATTTGGTAAT	CA : 146
			440	*	460		80
TrMDHh1		TTCCTGCTGGTGT	TCCCCCTAAAC	CTGGAATG	ACAAGAGATGA	CTCTTCAATATAAA	TG: 479
TrMDHh2	:	THE CONTRACT CONTRACT	<b>゙゙゙゙゙゙゙゙゙゙゙゚゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚ヹ゚</b>	CTCCAANC	ACAAGAGAIGA.	ICICITICHMINING	. 220
TrMDHh3		TTCCTGCCGGTGT	TCCCCGTAAAC	CTGGAATG	ACAAGAGATGA'	CTCTTCAATATAAA	re : 206
		*	500	*	520		40
TrMDHh1		CCGGGATCGTTAA	AACACTCTGTC	BAAGCAATT	GCGAAGCGATG	TCCTAAGGCGATTGT	CA : 539 CA : 310
TrMDHh2			A A CA CHOMOTO	マカ かこぐる みでで	CCAAAGCGATG	TCCTAAGGCGALIGI	G5 : 310
TrMDHh3	. :	CCGGGATCGTTAA	AACACTCTGT	AAGCAATT	GCAAAGCGATG	TCCTAAGGCGGTTGT	. 500
		*	560	*	580	* 6	500
TrMDHh1		ACGTGATTAGTA	TCCGGTTAAC'	CCACTGTC	C	TO A COTTOTO A A A	: 572 AG : 370
TrMDHh2		: ACGTGATTAGTA	ATCCGGTTAAC'	TCCACTGTC	CCCATTGCGGC	TGAAGTTTTCAAAAC TGAAGTTTTCAAAAC	
TrMDHh3	3	: ACGTGATTAGTA	VICCGGTTAAC	ICCACTGTC	DDDJD111AJJJJ.		

						•			
			*	620	*	640	*	660	
TrMDHh1	:						2AWGTIGGTTG	SGGCCA	: - : 430
TrMDHh2 TrMDHh3	:	CCGGTAC'	TTATGA' TTATGA'	rcccaagagact rcccaagagact	TTTGGGAGT TTTGGGAGT	GACAATGCTT(	GATGTGGTTC	GGGCCA	: 386
1111011113	•	00004110							
			*	680	*	700	*	720	
TrMDHh1	:								: -
TrMDHh2	:	ATACGTT	TGTGGC'	TGAAGTTCTTGG	TCTTGATC	CAAGGGATGTG	GATGTCCCAG CATGTCCCAG	TTGTCG	: 490 : 446
TrMDHh3	:	ATACGTT	TGTGGC	IGAAGTTCTTGG	TCTTGATC	LAAGGGAIGIG	GAIGICCCAC	110100	
								780	
m2mm/2 =			*	740	*	760 			: -
TrMDHh1 TrMDHh2	:	GAGGACA	TGCCGG	AATCACCATTTI	ACCTCTGC	TTTCTCAGGTT	AAACCACATT	CCTCTT	: 550
TrMDHh3	:	GAGGACA	TGCCGG	AATCACCATTTI	'ACCTCTGC'	TTTCTCAGGTT	AAACCACATI	CCTCTT	: 506
			*	800	*	820	. *	840	_
TrMDHh1	:	mon don d		7 7 CT CT 7 CT 7	<b>7</b>				: 576
TrMDHh2 TrMDHh3	:	TCACGAC	'AAAGGA 'AAAGGA	AATTGAGTACTI AATTGAGTACTI	GACAGATC	GCATACAAAAC	GGTGGAACT	AAGTTG	: 566
			*	860					
TrMDHh1	:				· <b>-</b> : -				
TrMDHh2					: -				
TrMDHh3	:	TTGAGGC	CAAAGC	TGGAGCTGGCT	<b>E</b> : 592				

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		*	20 *	•	40	*	60		
TrMDHi	:	GNAATCCTCTTTGNCTCC		TTTTTTC	CTTCCTTCTTAC	ACCTTCTC'	LTA	:	60
********	•								
		*	80 *	• 1	100	*	120		
TrMDHi	:	TCAACTTTCCACCTCTGA		ATCTTTTC?	<b>CATTTTCTTAT</b>	ACCCTTTT	ACA	:	120
	٠								
		· * 1	40		160	*	180		
TrMDHi		AACTTCTTCATAAAGTGT		TATTACT	CTTTTCAAGAAC	CACAAAAA	CAG	:	180
	Ī								
		* 2	00		220	*	240		
TrMDHi	:	TGTTTCTTGAATTCTTTG		TCCTGCA	ACCATGGCCTTG	GCACACTT	AAA	:	240
		•			•				
		* 2	60 *	* :	280	*	300		
TrMDHi	:	CAACCCCACTTGCTCAAA	AACTCAACTTC	ACTCATCA	CAACTCTCATTI	CTCTCTAG	GAC	:	300
			20 1		340		360		
TrMDHi	:	TCTCCCTAGGCAATATCA	CTGTACTTTTG	CACCACTT	CACAGAACTCAA	CATGGCAG.	TAA	:	360
			80		400		420		
TrMDHi	:	TACTTGTTCTGTTGCACC	AAATCAAGTGC	AGGCTCCA	GCTGTACAATCA	CAGGATCC	CAA	:	420
			40 .		460		480		
TrMDHi	:	GAATAAGCCTGATTGCTA	TGGTGTCTTCT	GCCTTACC'	TATGATTTGAAG	GCTGAAGA	GGA	:	480
		• •							
	•	_					- 4 0		
			00		520 		540		540
TrMDHi	:	GACAAAATCCTGGAAGAA	ATTAATCAACA:	TTGCAGTC	TCAGGTGCTGCT	GGAATGAT	TIC	:	240
			<b>60</b>		<b></b>	•	600		
mas mar		* 5 CAATCATCTACTTTTCAA	60		580 ﺳﯩﺴﯩﺮﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪﯨﺪ				600
TrMDHi	:	CAATCATCTACTTTTCAA	GCTTGCATCTG	GIGNAGII.	1 1 1GGCCCWWW1	.caacciai	100	•	
		* 6	20	*	640				
TrMDHi		GCTGAAATTATTAGGATC				647		•	
*******	•	OCTOWNTINITYGGATC							

\* 20 \* 40 \* 60
Trmdhi : MALAHLNNPTCSKTQLHSSQLSFLSRTLPRQYHCTFAPLHRTQHGRITCSVAPNQVQAPA : 60

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\* 80 \* 100 \* 120 TrMDHi : VQSQDPKNKPDCYGVFCLTYDLKAEEETKSWKKLINIAVSGAAGMISNHLLFKLASGEVF : 120

\* 140

TrMDHi : GPNQPIALKLLGSERSFQALEG : 142

rigure 81 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHi

TrMDHi1 TrMDHi2	:	* 20 * 40 * 60  GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTCCTTCCTTCTTACA-CTTCTCTTAT  TTCTTAGACCTTCTCTTAT	:	60 19
TrMDHi1 TrMDHi2		* 80 * 100 * 120 CAACTTTCCACCTCTGAACAAACTTCHATCTTTTCTCATTTTCTTATACCCTTTTAGAAA -AACTTTCÑACCTCTGAACGAAA -TT -AATCTTTTCT -ATTTTCTTATACCCTTTTACAAA	:	121 76
TrMDHil TrMDHi2	:	* 140 * 160 * 180 CTTCTTCATAAAGTGTTATTTTTTTTTTTTTTTTTTTTT		180 137
TrMDHi1 TrMDHi2	:	* 200 * 220 * 240  TTCTTGAATTCTTTGÜAATTTTTTTTTTCCTGCAACCATGGCCTTGGCACAGTTAAACAAT  TTCTTGAATTC TTGGAA TTTTTTTTTCCTGCAACCATGGCÜTTGGCACACTTAAACAAC	:	241 196
TrMDHi1 TrMDHi2	:	* 260 * 280 * 300  CCCACTTGCTCAAAAACTCAACTTCACTCATCACAACTCTCATTTETCTCTAGGACTCTCC  CCCACTTGCTCAAAAACTCAACTTCAETCATCACAECTCTCATTTCTCTCTAGGACTCTCC	:	302 257
TrMDHi1 TrMDHi2	:	* 320 * 340 * 360 CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG	:	363 318
TrMDHi1 TrMDHi2	:	* 380 * 400 * 420  TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG  TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG	:	424 379
TrMDHil TrMDHi2	:	* 440 * 460 * 480 CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGAGACAAAAT CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGAGACAAAAT	:	485 440
TrMDHi1 TrMDHi2	:	* 500 * 520 * 540 CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCAGTGATGATTTCCAATCATCT CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT	:	546 . 501
TrMDHil TrMDHi2	:	* 560 * 580 * 600 * ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGTCCAAATCAACCTATTGCGCTGAAATTA ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGCGCTGAAATTA	:	602 562
		620 * 640  TTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 599		

··		* 20 * 40	*	60		
TrMDHi	:	GCAAAGCNCTCNCNGACCTGGTGTGGAGCGAGCAGCTTTGCTAGA	ACATAAATGGGC	AGAT	:	60
		* 80 * 100	*	120		
TrMDHj	:	TTTTGCGGAGCAGGGAAAAGCTCTAAATGCAGTCGCATCTCGCAA	ATGTCAAAGTTA'	ragr	:	120
			•			
		* 140 * 160		180		
m>-m714		* 140 * 160 TGTGGGAAACCCTTGCAATACAAATGCATTAATATGCTTGAAGA	ልጥ <b>ርርጥር</b> ርል አልጥል'			180
TrMDHJ	:	TGTGGGAAACCCTTGCAATACAAATGCATTAATATGCTTGAAGA	11001001222			
		* 200 * 220	*	240		
TrMDH	:	TGCAAAAATTTTCATGCTTTAACCCGTTTAGATGAGAACAGAG	CAAAATGTCAGC	TAGC	:	240
•						
		* 260 * 280	* **	300		300
TrMDHj	:	CCTCAAGGCAGGTGTCTTCTACGATAAAGTGTCGAATATGACGA	TATGGGGAAACC.	ACIC	•	300
		* 320 * 340	*	360		
т∽мон∹		: AACTACTCAGGTCCCCGATTTCTTAAATGCCAGAATCGATGGTT	TGCCTGTCAAAG	AAGT	:	360
111111111	•	· PRIOTIGIONO I CONTRA LA				
		* 380 * 400	*	420		
TrMDHj	:	: GATTAAGGATCAAAAGTGGTTAGAGGAAGAGTTCACCGAAAAAG	TTCAAAAGAGAG	GTGG	:	420
		* 440 * 460	*	480		
		* 440 * 460 : CGTGCTTATTCAAAAGTGGGGAAGATCGTCTGCTGCATCAACTT			:	480
נמשויוו	•	: CGIGCIIAIICAAAAGIGGGAAAGAICGICIGCIGGAIGAIGA				
		* 500 * 520	*	540		
TrMDHj	:	: TGCCATACGATCTTTGATCACTCCTACTCCGGAGGGTGATTGGT	TTTCTACTGGTG	TGTA	:	540
			•			
masenti-i		* 560				
LEMDHJ	:	: TACAGCTGGAAATCCTTATGGAATAGCTG : 569				



\* 20 \* 40 \* 60 TrmDHj : QSXXXPGVERAALLDINGQIFAEQGKALNAVASRNVKVIVVGNPCNTNALICLKNAPNIP : 60

\* 80 \* 100 \* 120

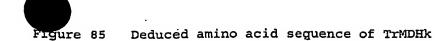
TrmDHj : AKNFHALTRLDENRAKCQLALKAGVFYDKVSNMTIWGNHSTTQVPDFLNARIDGLPVKEV : 120

\* 140 \* 160 \* 180

TrMDHj : IKDQKWLEEEFTEKVQKRGGVLIQKWGRSSAASTSVSIVDAIRSLITPTPEGDWFSTGVY : 180

TrMDHj : TAGNPYGIA : 189

TrMDHk :	* GNGTAGAACCC	20 GTGAAGCCTT	* FTCCCTCCGG1	40 PCTCCCCGCTTC	* GCGCCGTCGCCG	60 TCAATT	:	60
TrMDHk :	* GCTGCTTGTGT	80 CGTCGCCTCC	* AGCTCCTCCTC	100 CCTCCACTGTGC	* CCAACCGAATTA	. 120 CAAACC	:	120
TrMDHk :	* AAAAAAATGGC	140 GACTTGTTTG	* CAAACACAAC1	160 CCTCCACACA	* AGACCTTTTCAG'	180 TTTCGG	:	180
TrMDHk :	* TCTTCCTCGTC	200 GACAAGACCAI	* ACTTCCCTAAG	220 ATGTTCCGCC	* GCCACCCCATCC:	· 240 ACCAAA	:	240
TrMDHk :	* AAATCCTACAA	260 AATCACTCTTO	* CTTCCGGGTGA	280 TGGCATAGGTO	* CCTGAAGTCGTT	300 TCCGTC	:	300
TrMDHk :	* GCTAAAGACGT	320 TCTTCTCCTC!	* ACTGGATCCAT	340 CCATGGGATTA	* \AACTTGAGTTT(	360 CAAGAG	:	360
TrMDHk :	* AAGCTTTTGGG	380 IGGTGCTGCT(	* CTTGATGCTAC	400 TGGAGTTCCTI	* TACCTGATGATA	420 ACTCTT	:	420
TrMDHk :	* TCTGTTGCTAA	440 GCAATCTGATO	* CTGTTCTTCT	460 TGGTGCTATTG	* GAGGGTATAAA1	480 rgggat	:	480
TrMDHk :	* AAAAATGAGAA	500 ACAGCTGAAGO	* CAGAAACTGG	520 ATTGCTTCAGO	* TACGAGAAGGG	540 CTTCAA	:	540
TrMDHk :	* GTTTTTGCTAA	CTCAGA : 5	58					



TrmDHk : MATCLQTQLLHTRPFQFRSSSSTRPTSLRCSAATPSTKKSYKITLLPGDGIGPEVVSVAK : 60

120 80 \* · 100 TrmDHk : DVLLLTGSIHGIKLEFQEKLLGGAALDATGVPLPDDTLSVAKQSDAVLLGAIGGYKWDKN : 120

140

TrMDHk : EKQLKPETGLLQLREGLQVFANLR : 144

		*	20	*	40	*	60		
TrPEPCa	:	GNNACATTNCCGAA	TGCTGCTGAAC	TAGGGAGTG	ATTCCCTTGGI	AGCCTATGTCA	TCTCT	:	60
		* ATGGCCTCAAGTGC	80	*	100 አርረምምምንሪ	* => >CC>TCC>C	120 'GTCTT		120
TEPEPCa	:	ATGGCCTCAAGTGC	AAGCGAIGICC	TIGCAGIAG	WGC1111WCW	<i>JAAGGA I GCAC</i>	.01011	•	120
•			140	•	160	•	180		
TrPEPCa	:	ACAGTTTGTGGAGA	140 ATTAGGAAGAG	: CATGTCCGG		rcgggrggttc		:	180
		*	200	*	220	*	240		
TrPEPCa	:	TTTGAAACTGTGCA	AGACCTGAGAG	GAGCTGGTG	CAGTTATCAG	AAAACTTTTAT	CAATC	:	240
•									
m-pena-		* GATTGGTACCGCCA	260	* \	280	* ^ C	300 TCGGT		300
Trpspca	:	GATTGGTACCGCCF	ACACATCATT	MGAACCAIA	ACGGACACCA	AGAGGI IAIGC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	•	500
		*	320	*	340	*	360		
TrPEPCa	:	TATTCTGATTCTG		GGCGCTTTA		GGAACTTTACA		:	360
		*	380	*	400	*	420		
TrPEPCa	:	CAAGAGGATGTAGT	GGCTGCTTGC!	ATAAGTACG	ATACTAAGGT	TACTTTGTTCC	CACGGC	:	420
TrPEPCa		* CGCGGAGGGAGTAT	440 TGGACGTGGC	* =GAGGCCCAA	460 CATATCTGGC	* TATTCAGTCCC	480 AGCCA	:	480
122 22 00	•								
		*	500	*	520	*	540		
TrPEPCa	:	CCTGGCTCTGTGAT	GGGAACCCTT	CGGTCAACTG	AGCAGGGAGA	GATGGTGCAGG	CCGAG	:	540
m		* TTTGGGTTGCCAC	560 ·	* *	580	* *	600		600
TrPEPCa	:	TTTGGGTTGCCACA	GACAGCAGT17	AGACAACTIG	AAATATACAC	AACAGC 1G1GC	JACII	٠	800
			620		640	* .	660		
TrPEPCa	:	GCTACACGTCGTC		CCTCGAGAAG		TAATCTAATGO		:	660
		•							
		*	680	*	700	*			
TrPEPCa	:	ATNTCAAAAATCAC	TTGTCAGTCC	PACCGCAGTG	TAGTCTATGA	AAATCCAGN :	713		

TrPEPCa	:	* 20 * 40 * 60 XTXPNAAELGSDSLGAYVISMASSASDVLAVELLQKDARLTVCGELGRACPGGTLRVVPL:	60
TrPEPCa	:	* 80 * 100 * 120 FETVQDLRGAGAVIRKLLSIDWYRQHIIKNHNGHQEVMVGYSDSGKDAGRFTAAWELYKA :	120
TrPEPCa	:	* 140 * 160 * 180 QEDVVAACNKYDTKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAE:	180
TrPEPCa	:	* 200 * 220 * : FGLPQTAVRQLEIYTTAVLLATRRPPLPPREEKWRNLMEDXSKISCQSYRSVVYENP : 23	17

Figure 88 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCa

	*	20	*	40 .	*	60	60
TrPEPCa1 :	GNNACATTNCCGA	ATGCTGCTGAACT	AGGGAGTGA'	TTCCCTTGGAG	CCTATGTCATC		-
TrPEPCa2 :						:	-
TrPEPCa3 :							
			•				
	*	80	* .	100	*	120	
TrPEPCa1 :	ATGGCCTCAAGTG	CAAGCGATGTCCT	TGCAGTAGA	GCTTTT-CAGA	AGGATGCACG	CIT	L19 27
TrPEPCa2 :				ACTTTTACAGA GCTTTTACAGA	MODITIOCHCO:		26
TrPEPCa3 :				GC'1"1"1"TACAGA	ing CHCG:	C.L.	
	•						
		140	*	160	*	180	
TrPEPCa1 :	gchigetatitegag	NGREGCCAAGAGC	ATGTCCIGG	TGGAACGUTGC	GGGTIGTECC'	rcta :	179 87
TrPEPCa2:		$\lambda$ $\lambda$ $\tau$ $\tau$ $\tau$ $\lambda$	ATGICCGG	LOGHMCGCTTC			86
TrPEPCa3 :	ACAGTTTGTGGAG	AATTAGGAAGAGC	ATGTCCGG	STGGAACGCTTC	GGG 1GG 1 TCC	icia.	
	*	200	*	220	*	240	
TrPEPCal :	TTTGAAACTGTGA	INCONCETNAGAGE	GAGCTGGTE	CAGTTATCEGE	AAACTTTTATC	GATA:	239 147
TrPEPCa2		12 2 C2 CCTC 2 C2 C(	2 (4) (4) (4) (4) (4)	AGILALCAGA			146
TrPEPCa3 :	TTTGAAACTGTGC	AAGACCIGAGAGC CAAGACCTGAGAGC	BAGCTGGTG	CAGTTATCAGAZ	MAMCILITATE		
	*	260	*	280	*	300	200
TrPEPCal	GACTGGTACCGT	AACACATCATTA	agaacca'ga	AŢŢGGACAŢŢCAA	GAGGTTATGGT	EGGE :	299 207
TrPEPCa2	AS MERCANDA CCCCC	¬' እ አርእርእጥር Δጥኘል.	AGAACCATA	ACGGACACCAA	OMOO : :::-		206
TrPEPCa3	GATTGGTACCGC	CAACACATCATTA	AGAACCATA	ACGGACACCAA	07.0012.77		
		•					
	*	320	*	340	*	360	359
TrPEPCal	: TATTCTGATTCG	GGTAAAGATGC <u>I</u> G	GCCCTTCA	CTGCTGCTTGG	GAACTTTACAA	AAGCT :	267
TrPEPCa2		GGTAAAGATGCEG GGTAAAGATGCCG GGTAAAGATGCCG		CIGCIGCIIO			266
TrPEPCa3	: TVAVETCITGATIVECT	GGIAAAGAIGCCG	000002				
						420	•
	*	380	*	400	A CACTETTIC		419
TrPEPCal	: CAGGAGGATGTT	GTAGCTGCTTGCA GTGGCTGCTTGCA	ATGAIITALIC	ATACTAAGGTI	ACTTTGTTCC	ACGGC :	327
TrPEPCa2	: CAAGAGGATGTA	GTGGCTGCTTGCA GTGGCTGCTTGCA	ATAAGTAC	SATACTAAGGTT	ACTTTGTTCC	ACGGC :	326
TrPEPCa3	CAAGAGGATGIT						
				4.60	*	480	
	*	440 ATTGGICGAGGI	*	460	TATTCAGTCCC		479
TrPEPCa1		an mmc ヘカ へつかんにい		ALAIGIGG.	1711777777		387
TrPEPCa2 TrPEPCa3	: CGCGGAGGGAGI	ATTGGACGTGGCC	GAGGCCCA	ACATATCTGGC'	TATTCAGTCCC	AGCCA :	386
HEBECAS	. 666						
				520	*	540	
	*	500 GATGGGAACACTT	regrenia en	GAGCAGGGAGA	AATGGTAGAGG	CCAAG :	539
TrPEPCa1		'' ''' ''' '' '' '' '' '' '' '' '' '' '	CHECK IN MANAGEMENT	17A17CACCCACA	OM TOO # - 0		447
TrPEPCa2 TrPEPCa3	: CONGGOTOTOTO	GATGGGAACCCTT GATGGGAACCCTT	CGGTCAACT	GAGCAGGGAGA	GATGGTGCAGG	CCGAG :	446
LL DE COO							
			*	. 580	*	600	
mac was a second	*	560 ACAGAÏJAGCIJGTT	AGACAACTT	GANIN	,		576
TrPEPCa1 TrPEPCa2		,	י ארט אר ארדיד	CAAATATACAC	AACAGCTGTGC	TACTT	: 507
TrPEPCa3	TTTGGGTTGCC	ACAGACAGCAGTT ACAGACAGCAGTT	AGACAACTI	GAAATATACAC	AACAGCTGTGC	MAT CALL	: 506
- · · · · · · · · · · · · · · · · · · ·							

		•		• .	40	*	60		
		* GNAAGGGACAAGCT	20		º™╱╱╱ͲϠ\ͲϹͲ(	ግግጥ አርርጥር <mark>አጥ</mark> ርር	CTAT :		60
TrPEPCb :		GNAAGGGACAAGCT	CTATCGTACTC	GTGAGCGGTC	'TCGCIVICT	CIIMOCIONIC			
			80	*	100	*	120		
		*	80	man adan man	የጥር እጥር እርብጣ	CTTGGAACCTC	TGAA:	:	120
TrPEPCb	: .	* TCTGAAATTCCTG	AAGAAGCCACAT	TCACCGAIG	LIGHTOHOTT				
									•
			140	*	160	*	180		
		*	740	and chick act	TGCGATTGC	CGATGGAAGCC	TTCTT	:	180
TrPEPCb	:	* CTATGCTACAGAT	CACTCTGTGCT	GIGGIGATE	31000:11-00				
					•				
		•					240		
		*	200	*	220	<b>*</b>			0.4.0
		GATTTCTTGAGGC	2 2 CHAMBACC 2 CALL	гттGGACTGT	CACTGGTAAG	BACTTGATATAA	GGCAA	:	240
TrPEPCb	:	GATTTCTTGAGGC	AAGIIICCACI.			•			
						_			
		•			200		300		
		*	260	*	280				300
m-pench		* GAGTCAGATCGTC	ACACGGACGTG	ATGGATGCCA	TTACCAAAC	ATTTGGAAAT IC	GMICC	•	500
TrPEPCb	•	GAGICAGAICCIC							
				•	340	*	360		
		*	320			<u>ረጥረ አርጥጥር</u> ርጥፕ(	GCAAA	:	360
TrPEPCb	•	* TACCAAGACTGGT	CTGAAGAAAAA	AGACAGGAA'I	GGCTTTTGT	CIGMGIIGGII			
111270	·					•			
		-	•						
			380 .	*	400	*	420		
		•	300	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	ΑΤΤΑΔΔΩΤΤΑ	GAGAAGTTTTAG	BAGACA	:	420
TrPEPCb	:	* AGGCCGCTTTTTC	3GACCTGACCTA	CCTCAAACCC	NI CHIMIN				
									•
						_	480		
		*	440 '	*	460	*			480
		* TTTCATGTCATA	CCACAACTTCC	TCAGACAAC'	TTTGGAGCCT	'ATATCATTTCG	ATGGCA	:	460
TrPEPCb	:	TTTCATGTCATA	GCHOMICIACO						
					520	*	540		
		*	500	*	520			٠. •	540
TrPEPCb		* : ACTGCCCCGTCT	GATGTGCTAGC	GTTGAACTT	CTTCAACGIC	AATGCAAAATC	Lucier	•	
TERRECO									
			•						
			560	*	580	*			
		*	560			ZAGTCTGCTCCI	GCTG:	5	598
TrPEPCb	)	* : CCGTTAAGAGTT	GTTCCGTTGTT	I GAGAAAC I I	GCTGWTCTC				

\* 20 \* 40 \* 60

Trpepcb : Xrdklyrtrersryllahgyselpeeatftdvdefleplelcyrslcacgdraiadgsll : 60

\* 80 \* 100 \* 120

Trpepcb : Dflrqvstfglslvrldirqesdrhtdvmdaitkhleigsyqdwseekrqewllselvgk : 120

\* 140 \* 160 \* 180

Trpepcb : Rplfgpdlpqtdeirevletfhviaelpsdnfgayiismatapsdvlavellqreckikn : 180

TrPEPCb : PLRVVPLFEKLADLESAPA : 199

rgure 91 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCb

TrPEPCb1 TrPEPCb2	:	* GNAAGGGACAAGCT GĪĀAGGGACAAGCT	. 20 CTATCGTACTC	* GTGAGCGGTC GTGAGCGGTC	40 TCGCTATCTC TCGCTATCTC	* TTAGCTCATGC TTAGCTCATGC	60 CTAT :		60 60
TrPEPCb1 TrPEPCb2	:	* TCTGAAATTCCTGA TCTGAAATTCCTGA	80 AGAAGCCACAT AGAAGCCACAT	* TCACCGATGT TCACCGATGT	100 TGATGAGTTO TGATGAGTTO	* CTTGGAACCTCT	120 TTGAA :		20 20
TrPEPCb1 TrPEPCb2	:	* CTATGCTACAGATC CTATGCTACAGATC	140	*	160	* CGATGGAAGCC	180 FTCTT :	-	.80 .80
TrPEPCbl TrPEPCb2	:	* GATTTCTTGAGGCA GATTTCTTGAGGCA	200 AGTTTCCACTI AGTTTCCACTI	* TTGGACTGTO	220 CACTGGTAAG CACTGGTAAG	* ACTTGATATAA ACTTGATATAA	240 GGCAA :		240 240
TrPEPCb1 TrPEPCb2	:	* GAGTCAGATCGTCA GAGTCAGATCGTCA	260 ACACGGACGTGA ACACGGACGTGA	* ATGGATGCCA ATGGATGCCA	280 TTACCAAACA TTACCAAACA	* TTTGGAAATTG TTTGGAAATTG	300 GATCC:		300 300
TrPEPCb1 TrPEPCb2	:	TACCAAGACTGGT(	320 CTGAAGAAAAA CTGAAGAAAAA	* AGACAGGAAT AGACAGGAAT	340 GGCTTTTGTC	* TGAGTTGGTTG TGAGTTGGTTG	360 GCAAA GCAAA		360 360
TrPEPCb1 TrPEPCb2		AGGCCGCTTTTTG	380 GACCTGACCTA GACCTGACCTA	* CCTCAAACCG CCTCAAACCG	400 ATGAAATTAG ATGAAATTAG	* GAGAAGTTTTAG	420 BAGACA BAGACA	-	420 420
TrPEPCb1		* TTTCATGTCATAG TTTCATGTCATAG	440 CAGAACTTCCA CAGAACTTCCA	* TCAGACAACT TCAGACAACT	460 TTGGAGCCTA	* ATATCATTTCGA	480 ATGGCA ATGGCA	-	480 480
TrPEPCb1 TrPEPCb2	-	ACTGCCCGTCTG	500 ATGTGCTAGCG	* GTTGAACTTC	520 TTCAACGTGATCAACGTGA	* AATGCAAAATCI AATGCAAAATCI	540 AAGAAT AAGAAT		540 540
TrPEPCb1		* CCGTTAAGAGTTG CCGTTAAGAGTTG	. 560 STTCCGTTGTTI STTCCGTTGTTI	* GAGAAACTTC	580 SCTGATCTCG SCTGATCTCG	* AGTCTGCTCCT	GCTG:	59 58	

			•						
		*	20	*	40 	* CTTAGTTAG	60 TTA	:	60
TrPEPCc :	GTCACATGA	CAAACNAT	ATCTCCCTTTC	CTAACTC	CGTGATCAAGGC				
		*	80	* -	100	*	120	_	120
TrPEPCc :	CACAAATTG	CTGTTAGG	TTTCGTTGTAC1	rttcccgt(	GCAATCCATAGT	ATCTTGGAC	3GAA	•	120
		*	140	*	160	*	180	•	180
TrPEPCc :	CAAACTAGA	ATTTTCCAC	CTAGGTCGTCA	CGAGATTT	TCCTCTTCACTA	TTTTTT	1110	•	100
		*	200	*	220	*	240		240
TrPEPCc :	ATATAATA	CTCAACAC	TTTTTCTAGCT:	ACTTACTA	GTACTGTGTAA(	CACAAATTI	IMII	•	240
	·	*	260	*	280	* ግሞረች አሞጥር ሽ	300 GACT	•	300
TrPEPCc :	CATTATGG	CTACTCCT	CGCAACATTGAA	AAAATGGC	TTCAATTGATG(	JICAATIGA	Onci	•	
		*	320	*	340	★ NTCCCTTTTCCT	360 יייע מייי		360
TrPEPCc :	ACTAGCAC	CAAGGAAA	GTTTCTGATGAT	'GATAAAC'I	TGTCGAGTATG: ·.	AIGC11161	****		
		*	380	*	400	* ~~~~~~~~~~	420 בתיתרם	•	420
TrPEPCc	: GGATCGAT	TCCTTGAC	ATTCTTCAAGAI	TTGCATG	BAGAAGATATCA	GACAAACIC	, I I CA	•	120
		*	440	*	460	* አርን እ አጥጥርብ	480		480
TrPEPCc	: AGATTGTT	'ATGAGT'TA	TCGGCAGAGTA	rgaagggg	AGCTTAAGCCGG	AGAAAI 160	· .	•	100
		*	500	*	520	* maggaaaa	540 TCATT		540
TrPEPCc	: ACTTGGGA	ATATGCTI	'ACTGGTCTTGA'	rgctggag.	ATTCTATTGTTA	TWGCWWW.	LUNA	•	
		*	560	*					
TrPEPCc	: TTCTCATA	TGCTTAA1	TTGGCAAACTT	<b>GCAGAGN</b>	: 575				

\* 40 20 Trpepcc : MatprniekmasidaqlrllaprkvsDDDklveyDalllDRFLDilqDlhgeDirqTVQD : 60

100 80 .

Trpepcc : CYELSAEYEGELKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANLAE : 110

Figure 94 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCc

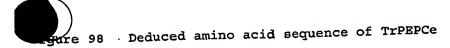
					·.		60		
		* GTCACATGACÜNACȚA	20	* TCTAACTC	40 CGTGATCAAGGCG	TTAGTTAGT		:	60
TrPEPCc1 TrPEPCc2	:	TGACAAGNA	TATCTCCCTTTC	TCTAACTC	CGTGATCAAGGCG	TTAGTTAGT	T'A	:	54
1112100-									
			80	*	100	* ]	L20		
TrPEPCc1		CACAAATTGCTGTTAG	GTTTCGTTGTAC	TTTCCCGT	GCAATCCATAGTA	ATCTTGGAGO	GAA	:	120
TrPEPCc2	:	CACAAATTGCTGTTAG	GTTTCGTTGTAC	TTTCCCGT	GCAATCCATAGT	ATCTTGGAG	AA	:	114
		*	140	*	160	*	180		
TrPEPCcl	:	CAAACTAGATTTTCC	ACCTAGGTCGTCA	CGAGATTT	TCCTCTTCACTA	TTTTTCTTT	TTC	:	180
TrPEPCc2	:	CAAACTAGATTTTCC	ACCTAGGT[]GTCA	CGAGATTT	TCCTCTTCACTA:	TTTTTCTTT'	MIC	:	174
					•				
		*	200	*	220		240		
TrPEPCcl	:	ATATAATAACTCAAC	ACTTTTTCTAGCT	'ACTTACTA	GTACTGTGTAAC	ACAAATTTT ACAAATTTT	ATT ATT	:	240 234
TrPEPCc2	:	ATATAATAA∏TCAAC	ACTITITICI AGCI	ACTIACIA	GIACIGIGIAAC	ACMMAL L L L			
			·						
		*	260	*	280		300 ACT	•	300
TrPEPCc1 TrPEPCc2	:	CATTATGGCTACTCC	rcgcaaca'i'i'ga <i>.</i> rcgcaacattga.	AAAATGGC AAAATGGC	TTCAATIGATGC	TCAATTGAG.	ACT	:	294
ILPEPCCZ	•	CHITATOGCIACICO							
					340		360		
TrPEPCc1		* ACTAGCACCAAGGAA	320 AGTTTCTGATGA	GATAAACI				:	360
TrPEPCc2	:	ACTAGCACCAAGGAA	AGTTTCTGATGA	rgataaact	TGTCGAGTATGA	TGCTTTGTT	ATT	:	354
		*	380	*	400	*	420		
TrPEPCc1	:	GGATCGATTCCTTGA	CATTCTTCAAGA!	TTTGCATG	BAGAAGATATCAG	ACAAACTGT	TCA	:	420
TrPEPCc2	:	GGATCGATTCCTTGA	CATTCTTCAAGA:	TTTGCATG	BAGAAGATATCAG	ACAAACTG1	TCA	•	414
		*	440	*	460	*	480		480
TrPEPCc1	:	AGATTGTTATGAGTT AGATTGTTATGAGTT	'ATCGGCAGAGTA' 'ATCGGCAGAGTA'	TGAAGGGG <i>I</i> TGAAGGGG <i>I</i>	AGCTTALLGCCGGA AGCTTAAGCCGGA	GAAATTGGA GAAATTGGA	GGA	:	474
TrPEPCc2	:	AGAIIGIIAIGAGII	ATCGGCAGAGIA						
	٠				500		540		
T~DEDCa1		* ACTTGGGAATATGCT	500 TACTCCTCTTGA	* TGCTGGAG/	520 ATTCTATTGTTAT	AGCAAAATC	TTA	:	540
TrPEPCc2	:	ACTIGGGAATATGCT ACTTGGGAATATGCT	TACTGGTCTTGA	TGCTGGAG	ATTCTATTGTTAI	AGCAAAATC	CATT	:	534
		*	560	*					
TrPEPCc1	:	TTCTCATATGCTTAA		GGCAGAGN					
TrPEPCc2	:				: 537				

					•	_		
		*	20	*	40	*	60	
m-pmpc4 .	አርአ <b>አር</b> ልጥርጣ	CATGTTTG	AGTTGTCTATGT	GGCGCTGC	AACGACGAGCT	CCGTGTTAG	AGC :	60
TPPEPCG :	AGAAGAICI							
			80	*	100	*	120	
		* 	BO CCTCAAAGAAA	*************	CATTATATTGA	GTTTTGGAA	ACA:	120
TrPEPCd :	TGAAGAGC'	FTCATAGAT	CCICAAAGAAA	MIGCINE				
					1.00	*	180	
	•	*	140	*	160	 		180
TrPEPCd :	GATTCCTC	CAAACGAGC	CATATCGTGTT	ATTCTTGG/	AGGTGTGAGGGF	CHARCIGIA	TIME .	
					•		240	
		*	200	*	220	*	240	240
യ∞ല്ലാലർ ം	тасасстс	AACGTGCT	ZGACAGTTATTA	GCAAATGG:	AACCTCTGACA:	CCTTGAAG	AGAC :	240
HPEPCU .	Inches				·			
			•					
		*	260	*	280	*	300	
	3 3 CCMCC3	 ሮርኒ እ አጥርያጥባህ	260 GAGCAGTTTCTG	GAGCCTCT	TGAACTGTGTT	ATAGGTCAC'	rttg :	300
Trperca	: AACCIICA	CGAALGII	011001101111					
					•			
			320	*	340 .	*	360	
			TCAATAGCAGAC	CCAACCCT	TCTTGATTTCT	TGCGACAAG	TTTC :	360
TrPEPCd	: TGCATGTG	GTGACCGA	TCAATAGCAGAC	GCHLCCCI				
			•					
					400	*	420	
		*	380	* ~- maac	╅┖╜┇╓┇╓╓ ┱╓┇┇┎┇╓╓┎┇		CAGA :	420
TrPEPCd	: TACATTTO	<b>3GACTTTCA</b>	CTTGTAAGACTC	GACATCCG	STCAMGAGICAG	ACACCCI.	, •••••	
							480	
		*	440	*	460	* = ==================================		480
TrPEPCd	: CGTTATG	SATGCAATT	ACAAAACACTTO	GAGATTG	SATCTTACCGAG	AATGGTCGC	MAGA :	400
1112100	• • • • • • • • • • • • • • • • • • • •							
							- 40	
		*	500	*	520 <sub>.</sub>	*	540	540
m~npnca	. ACCCACG	CAGGAATGG	CTCTTGTCTGA(	CTTAGTG(	GAAAACGCCCTC	TCTTCGGC	:ATGA	540
TIPEPCU	: ACGCAGO	CACCIAIT -						
			560	*	580	*	600	
		~ ~~~~~~~~~~~	AGAAATTGCCGA'	rGTTTTAG	ATACCTTNCAC	TNATTTCA	JAACT :	600
TrPEPCd	: TCTTCCT	AAGACAGA	AGMANI I GCCON.					
			630	*	640	*	660	
		*	620 rggtgcctatat	ርን ጥርጥር እ	TGGCAACCTCC	CATCTGAT	GTGCT :	: 660
TrPEPCd	: TNCCTCA	NATAGCTT.	IGGIGCCTATAT	CHICICHA	100012100100			
					•	•		
					700	*	720	
•		*	680	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	A COA COCCOTTA	አ <sub>እፕ</sub> ልርሞሞርሞሞ	CCACT	: 720
TrPEPCd	: AGCTGTC	GAGCTTTT.	680 ACAACGTGAATG	TCATGIGA	MGCMGCCGIIM			
					260	•	780	
		*	740	*	760			. 780
TrPEPCd	: GTTTGAA	AAGCTCGC	CNGTCTTGAGTC	TGCTCCTG	CTGCGGNAGCG	CGLLLLLLIN	TIMOM	. ,
						_	0.40	
		*	800	*	820	*	840	
m	. mmacan	יאאז א פיריכא	DOU NNTAATGGAAAN	CAGAAGTT	CNTGATAGGTAC	TCANACTNG	GGAAA	: 840
TTPEPCd	: TIGGGM	-uinwarcon	,		•			
			•					

TrPEPCd : AGATGCTGGCCGNN : 854

TrPEPCd :	EĽ	* DLMFELSMWRCNDELR	20 VRAEELHRSSKK	* DAKHYIEF	40 WKQIPPNEPYR	* VILGGVRDK	TAN eo	:	60
TrPEPCd :	TF	* RERARQLLANGTSDIL	80 EETTFTNVEQFI	* EPLELCY!	100 RSLCACGDRSIA	* DGSLLDFLR	120 QVS	:	120
TrPEPCd :	<b>: T</b> 1	* FGLSLVRLDIRQESDR	140 HTDVMDAITKHI	* Jeigsyre	160 WSEERRQEWLLS	* SELSGKRPLE	180 GHD	:	180
TrPEPCd :	: <b>L</b> ]	* PKTEEIADVLDTXHXI	200 SXLXSXSFGAY	* IISMATSP	220 SDVLAVELLQRI	* *	240 VVPL	:	240
TrPEPCd :	: F	* EKLAXLESAPAAXARI	260 XLDWXXTXXME	* SRSXDRYS	280 XXGKDAGX : :	283			

m~DEDCo ·		* GTTCACTGTCTCTCTG	20 NCCAATTTTCCT	* CCCTTGTC	40 TTCTTTTTCTTC	* TTCTTCCTC	60 GTA :		60
Trperce :	,								
TrDEDCe :		* TCTTACTGCCTCATTA	80 CACGGGTGAGAA	* .GGAGTGAA	100 TTGCTCCAATGG	* Caacaaaci	120 AAAA :	1	.20
				•		•			
TrPEPCe :		* TGGAAAAATGGCATC	140 CAATTGATGCACA	* \GCTTAGAC	160 AATTAGTACCAG	* CAAAAGTTI	180 AGTG :	: 1	L80
<b>Ͳ</b> ϫ₽ΕΡϹΑ :		* AAGATGATAAACTTAT	200 TGAGTATGATG	* TTTGTTG1	220 TGGATCGGTTTC	* CTTGATATC	240 CTTC	: 2	240
							300		
TrPEPCe :	:	* AGGATTTACATGGAGA	260 AGGATCTGAAAGI	* ATTCTGTT(	280 CAAGAAGTGTAT(			: :	300
TrPEPCe :	:	* AGTATGAAAGAAAGC	320 ATGATCCTAAGA	* AACTTGAA	340 JAGCTCGGAAAT	* TTGATAACA	360 AGTT	: ;	360
TrPEPCe	:	* TAGATGCAGGAGATT	380 CAATTGTTGTTG	* CTAAGTCC	400 TTTTCGCACATG	* CTTAACTTG	420 GCCA	:	420
TrPEPCe	:	* ACTTAGCTGAAGAGG	440 TTCAGATTGCTC	* ATCGTCGA	460 AGGAACAAGTTG	* AAGAAAGGF	480 AGATT	:	480
TrPEPCe	:	* TTAGGGATGAGAGCA	500 ATGCAACTACCG	* AATCAGAC	520 ATCGAAGAAACT	* CTTAAGAGA	540 ACTTG	:	540
TrPEPCe	:	* TGTTTAATATGAAGA	560 AATCTCCTCAGG	* łaagtinti	580 GATGCGTTGAAG	* SAACCNNACO	600 CGTTG	:	600
TrPEPCe	:	* ATTTGGTTCTTACTC	620 BCTCATCCCACTO	* CAGTCCGTI	640 CCGANGNCCNCTC	* SCTTCCCNN	660 NGCCT	:	660
TrPEPCe	;	* : GGNACGGGNACCGCI	680 NCTGNCTATCNN	* ACTGNNN :	: 693				



TrPEPCe :	:	* 20 MATNKMEKMASIDAQLRQLVPAKVS	* SEDDKLIEYI	40 DALLLDRFLDIL	* QDLHGEDLK	60 DSVQEV	:	60
TrPEPCe	:	* 80 YELSAEYERKHDPKKLEELGNLITS	* SLDAGDSIV	100 . Vaksfshmlnlæ	* NLAEEVQIA	120 HRRRNK	:	120
TrPEPCe	:	* 140 . LKKGDFRDESNATTESDIEETLKR	* LVFNMKKSP	160 QEVXDALKNXTV	* /DLVLTAHPI	180 QSVRXX	:	180

TrPEPCe : LLPXAWXGXRXXYXTX : 196

## gare 99 Consensus contig nucleotide sequence of TrCSa

		*	20	*	40	*	60		
rrCSa	: (	GNNNCNCNACCAT	TACATTAATNAC	ACTTTCCNCT	TTCGCCTTG'	TTCTTTCTCTT(	CTCAA :		60
		*	80	*	100	*	120		
TrCSa	:	TATAAAGACCAAT	TCAATTCCCAAT	rcttttgga1	CCGAAATCA	TTCATTCTACG	CGTCT :	•	120
			140	*	160	*	180		
TrCSa		TCTCTCTCTCTG	CGTTTCAAACCC	TAGTTGTTT		TCTAAATGGCG	TTCTT:		180
11000	•								
			200	•	220	*	240		
TrCSa		TCGAAGCGTTTCI	200 GCGCTTTCAAAA	CTACGATCT		AACAACCTAGI	CTTGC:		240
IICSa	•	1COMOCO 11101		•					
					280	*	300		
m=//Co		* TAATTCAGTTAGA	260 TGGCTCCAAACI	CCAAGCTCC		ATCTTTATTCT	GAGAT:		300
TrCSa	•	IAMITCAGITAGE	1100010011						
			252	•	340	*	360		
m . co.		* GAAGGAGCTAGTT	320 "CCAGAGTATCAG	GAACGTGTT.	AAGAAGTTG!	AGAAAGACCAT			360
TrCSa	:	GAAGGAGC TAGT	CCAGAGIAICA	.0.1100101					
			•		400	*	420		
maa-		* TGTTGAATTGGG	380 ************************************	* PGATATGGTA		ATGAGAGGAAT		:	420
TrCSa	:	TGTTGAATTGGG							
		•			460	*	480		
m		* TTTAGTGTGGCT	440 ***********************************	rgacccagat		CGCTTTAGGGG		:	480
TrCSa	•	111AG1G1GGC1	A00010:100101						
					520	*	540		
m00-		* AATTCCTGACTG	500 CCAGAAACACT	rccaggtgci	TTTCCTGGT	GGGGAGCCTTT	GCCCGA	:	540
TrCSa	:	AATICCIGACIG	CCACMERIC						•
					580	*	600		
m		GGCTATACTGTG	560 GCTTCTATTGAC	CGGAAAGGT	CCAAGTAAA	GAGCAAGTAGA	TTCATT	:	600
TrCSa	•	GGCIAIACIOIC			•				
•			500	•	640	*	660		
m~cc.		* AGCTCACGAATI	620 GCGAAGTCGTGC	AAAAATCCC	AGAGTATGCI	TACAAGGCAAT	TGATGC	:	660
TrCSa	•	AGCICACGARII							
			400		700	*	720		
m-cc-		* ACTGCCTGTTTC	086 PACCATCATC	GACACAATT	ragtactggi	CTAATGGCCCT	CCAGGT	:	720
TICSa		ACIGCCIGITIC	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,						
			=		· 760	*	780		
m., GC =		* : GGAGAGTGAGT	740 TTACAAAGGCAT	CGAGAGTGG	GATACATAA	TCAAGGTATT		:	780
TECS		GGAGAGIGAGI	171012 1100 01111						
				<b>.</b> .	820	*	840		
m - 00-		* : AACTTATGAGG	800 PTT	PAATTGCTCG	TTTGCCTGG	AATTGCTGCCT		:	840
Tress	1	: WWCITHIGWGG							
		•			880	*	900		
m-00-		* . maanaaanne	860 ACAAGGATGGAA	AAATCATACC	ATTGGATGA'	TTCTTTGGATT	-	:	900
TrCS	٠.	: ICGACGGATAT	nomodar domi						
					940	*	960		
m-ac	_	* : AAACTATGCTC	920 ACATGTTAGGAT	TTGATGATCC	AGAAACGCT	GGAGTTTATGA		:	960
TECS	CL.	: WWWCIWIGCIC							

\* 1000 \* 1020 980 TrCSa : TATTTCTATCCATAGTGATCATGAAGGNGGCAACGTTAGTTCTCACACAGCTCACCTAGT : 1020 \* 1040 \* 1060 \* 1080. TrCSa : TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG : 1080 1100 \* 1120 TrCsa : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 1140 1160 \* 1180 \* TrCSa : GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 1200 \* 1240 \* 1260 1220 TrCsa : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 1260

\* 1300 1280

TrCsa : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 1307

TrCSa	:	* MAFFRSVSALSKLRSRV	20 GQQPSLANSVRW	* ILQTPSSSN	40 TDLYSEMKELV	* PEYQERVKK	60 LKK :		60
TrCSa	:	* DHGSVELGKITADMVLG	80 GMRGMTALVWLO		100 IRFRGMTIPDC		120 GGE :	1	120
TrCSa	:	* PLPEAILWLLLTGKVPS	140 KEQVDSLAHELI	* RSRAKIPE\	160 YAYKAIDALPVS		180 GVM	:	180
TrCSa	:	* ALQVESEFTKAYESGIR	200 KSRYWEPTYED	* SLNLIARLI	220 PGIAAYIYRRIY	* KDGKIIPLĽ	240 DSL	:	240
TrCSa	:	* DYGANYAHMLGFDDPET	260 LEFMRLYISIH	* SDHEGNVS	280 SHTAHLVASSLS	* SDPYLAFAA!	300 ALNG	:	300
TrCSa	:	* LAGPLHGLANQEVLRW	320 IRNIVKEFGTPN	* (ISTEQLSD	340 YIHKTLNSGQV	* VPGYGHGVLI	360 RNTD	:	360
TrCSa	. :	* PRYTCOREFALKHLPN	OP : 378						

TrCSa : PRYTCQREFALKHLPNDP : 378

gure 101 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSa

		* 20 * 40 * 60		<b>C</b> 0
TrCSa1		GNNNCNCNACCATTACGTTAATHACAGTTTCCCCCTTCTTCTCTTCTC		60
TrCSa2		GNNNCNCNACCATTACGITAAIGACAGITICGCCTTGTTCTCTTCTCT	;	45
TrCSa2			:	-
	•		:	-
TrCSa4	:		:	-
TrCSa5	:		:	· <b>-</b>
TrCSa6	:		:	-
TrCSa7	:			
		* 100 * 120		
		* NII " 100		120
TrCSal	:	TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCAT	-	104
TrCSa2	:	TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCAT	•	40
TrCSa3	:	TARCENTANA - TONICH INCENTACT INCOME THE CONCERNCE INCOME	•	10
TrCSa4	:	TACCGAAA	:	TO
TrCSa5	•		:	-
TrCSa6	:		:	-
TrCSa7	:		:	-
II CSa /	•	·		
		* 140 * 160 * 180		
		TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTTTTTT	:	180
TrCSal	:	TO THE TOTAL PROPERTY OF A A COCTAGTT GTT GTT GAT TGAT TGAT TGAT TGAT T	:	164
TrCSa2		TCTCTCTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGA	:	100
TrCSa3		TCTTMCTTCTCTGCGTTTCAAACCCTAGTTGTTTTTTTTTT	:	67
TrCSa4		TNNITCGTHTCTAC-TTT-EMACCCT-GIIGITIAGIICAT TCATO	:	_
TrCSa5	:		:	_
TrCSa6	:			_
TrCSa7	٠ :		•	
		* 240		
				240
TrCSa1		TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC	•	224
TrCSa2		THE PARTY OF THE PROPERTY OF T	•	160
TrCSa3	3	TOCAN COCTETCTCCCCCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTGGC	•	127
TrCSa4	Ļ	TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC	•	12/
TrCSas			:	_
TrCSac			:	-
TrCSa7			:	-
II CDU		•		
		* 260 * 280 * 300		
m~∩c~:		TRANTICA CITAGA TGGCTCCA A CTCCA AGCTCCAGTA A CACTGA TCTTTATTCTGA GAT	:	300
Trcsa:		TA A TITICA CITTA CATGCCTCCA A A CTCCA A GCTCCAGTAACACTGATCTT TALTCIGAGAT	•	284
TrCSa		TO A BETTO COTTO CATEGORICA A ACTCCA AGCTCCAGTAACACTGATCTTTATTCTGAGAT		220
TrCSa:		: TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT	:	187
TrCSa		: TAATTCAGTTAGATGGCTCCAAACTCCAACTCCAACT	:	-
TrCSa!		:	:	-
TrCSa			:	_
TrCSa'	7	:,		
		•		
		. 340 * 360	ı	
		* 370 * 340	_	360
TrCSa	1	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGA		
TrCSa	2	GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGA		
TrCSa	3	GRAGA CONTROLL CARROLL CARRATCA CON A CONTROLL CARROLL		247
TrCSa	4	: GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGA		£4/
TrCSa			•	-
TrCSa			•	-
TrCSa			•	-
11034		•		

		* 400 * 420		
		* 380 * 400  TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC:	4	20
TrCSa1	:	TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC: TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGACAGCAATGACAGC	4	04
TrCSa2	:	TGTTGAATTGGGAAAAATCACAGCIGATATGGTACTTGGTGGAATGAGAGGAATGACAGC TGTTGAATTGGGAAAAGTCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACAGC TGTTGAATTGGGAAAAGTCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACAGC	3	40
TrCSa3	:	TGTTGAATTGGGAAAAGTCACAGCIGATATGGTACTTGGTGGAATGAGAGGAATGACTGC: TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC:	3	307
TrCSa4	:	TGTTGAATTGGGAAAAATCACAGCIGATATGGTACTTGGTGGAATGAGAGGAATGACTGC		51
TrCSa5	:	GNGGAAAAATAACAGCTGATATGGTACTTGGTAGATGACTGC		16
TrCSa6	:			-
TrCSa7	:			
		- · · · · · · · · · · · · · · · · · · ·		
		* 440 * 460 * 480		
		TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC	:	480
TrCSal	:	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC	:	464
TrCSa2	:		:	400
TrCSa3	:	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAÑATGAGGGAATTCGCTTTAGGGGCATGAC	:	367
TrCSa4	:	THE REPORT OF A COUNTY COUNTY COUNTY OF THE PROPERTY OF THE PR	:	111
TrCSa5	:	TTTAGTGTGGCT-GGCT-NGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC	:	74
TrCSa6	:	TTTAGTGTGGCT-GGCTGTGTGTGTGTGTGTGTGTGTGTGTGTG	:	-
TrCSa7	:			
		* 500 * 520 <b>*</b> 540		
TrCSa1	•	AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA	:	540
TrCSa2	-	A REPROCEED CONCLAINT A A CACTTCCAGGTGCTTTTCCTGGTGGGGGGCCTTTGCCCGA	:	524
TrCSa3		THE COURT OF THE C	:	460
TrCSa4		A ARTICOTO OTOCOA CA A A ACACTTGCAGGTGCTTTTNCTGGGGGGGGAGNCTT TGUCCUA	:	427
TrCSa5		A A DESCRIPTION OF COLOR CALADA CACTTCCAGGTGCTCTTCCTGGTGGGGAGCCTTTGCCCGA	:	171
		THE STATE OF THE S	:	133
Trusao	:	AATTCCTGACTGCCAG AAACACTTCCAGGTGCTTTTCCTCGTGTGTGT		
TrCSa6		AATICCIGACIGCCAGAAPIACHCTTCCAGGIGCTTTTCCTGGIGGGAGCCTTTGCCCGA	:	-
		AATTCCTGACTGCCAG-AAACACTTCCAGGTGCTTTTCCTGGCTGCTGCTGCCAG	:	-
		500:	:	-
		* 560 * 580 * 600·	:	600
TrCSa7	:	* 560 * 580 * 600°	:	- 600 584
TrCSa7 TrCSa1 TrCSa2	:	* 560 * 580 * 600 GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT	:	•
TrCSa7 TrCSa1 TrCSa2 TrCSa3	:	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT	: : : :	584
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4	:	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT		584 520
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4 TrCSa5	2 : 3 : 4 : 5 :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGCGGGTTTTTTATTGACCGGTA	:	584 520 456
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4 TrCSa5		* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT	: : : : : : : : : : : : : : : : : : : :	584 520 456 231
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4 TrCSa5		* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGCGGGTTTTTTATTGACCGGTA	: : : : : :	584 520 456 231
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4 TrCSa5		* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGCGGNTTNTATTGACCGGNN	: : : : : :	584 520 456 231
TrCSa7 TrCSa1 TrCSa2 TrCSa3 TrCSa4 TrCSa5		* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATCATT  GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATCATT  GGCTATACTGCGGTTTTTTTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT		584 520 456 231 193
TrCsa7 TrCsa1 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6	2 : 3 : 5 : 7 :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTGCGATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  * AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193
TrCsa7 TrCsa3 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa7	: 2 : : 3 : : 5 : : 7 :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGNN	: : : :	584 520 456 231 193 -
TrCsa7 TrCsa1 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6	: : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGNN	: : : :	584 520 456 231 193
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6 TrCsa6 TrCsa6 TrCsa6	: : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGNN GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCN AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6 TrCsa7 TrCsa7	1 : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCN AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6 TrCsa7 TrCsa7	1 : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCN AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa6 TrCsa7 TrCsa7	: : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGCGGTTTTTATTGACCGGNN  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	: : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGCGGTTTTTATTGACCGGNN  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	: : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	: : : : : : : : : : : : : : : : : : : :	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGCGGNTTNTATTGACCGGNN GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCN AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 - 291
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	1 2 3 3 3 5 5 7 1 1 2 2 3 3 5 5 6 7 1	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTECCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  * AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  * 680 * 700 * 720		584 520 456 231 193 - 660 588 580 291 253
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	123 ::::::::::::::::::::::::::::::::::::	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTTTTTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT   * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCTACAAGAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCTACAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC		584 520 456 231 193 - 660 588 580 291 253 -
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6	123 1557 123 1567 . 123	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTECCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTECCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAAGGTACCAAGTAAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT   * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCGAAGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCTAATGAAAAATCCCAGGTATTGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCTAATGAAAAATCCCAGGTATTGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCTAATGAAAAATCCCAAGTATGCTTACAAGGCCAATTGATGC  AGCTCACGAATTGCTAATGAAAAATCCCAAGTATTACAAAGTAATGCCCCCCCC		584 520 456 231 193 - 660 588 580 291 253 -
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa7	1234::::::::::::::::::::::::::::::::::::	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTECCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGNN  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT   * 620 * 640 * 660  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCACGATTTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC  AGCTCCTGTTTCTGCTCATCCAATGACACAAN  ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT  ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT		584 520 456 231 193 - 660 588 580 291 253 - 692 640
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa7	1234557 12345567 . 123455	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  * AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGATTTGCGAAGTCGTGCAAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT  * 680 * 700 * 720 **ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT **ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT **ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT		584 520 456 231 193 - 660 588 580 291 253 - 692 640 - 351
TrCsa7 TrCsa3 TrCsa4 TrCsa5 TrCsa6 TrCsa7	1234567 . 123456	* 560 * 580 * 600  GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGGTTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT  * 620 * 640 * 660  * AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCN AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC AGCTCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT		584 520 456 231 193 - 660 588 580 291 253 - 692 - 640 - 351 313

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TrCSa1 :						:	-
TrCSa2:	GGAGAGTGAGTTTA	CAAAGGCATAÜ	GAGAGTGGG	ATACATN		:	681
TrCSa3 :						;	-
TrCSa4:	GGAGAGTGAGTTTA	CAAAGGCATAC	GAGAGTGGG	SATACATAAGT	CAAGGTATTG	GGAGCC:	411
TrCSa5 :	GGAGAGTGAGTTTA	CANACCCAMAC	CNCDCTGGG	TATACATAAGT	CAAGGTALIG	GGAGCC .	373
TrCSa6:	GGAGAGIGAGIII		PAGAGTGG	A-NCNT-AGT	-AAGG-ATTG	GGAGCC:	34
TrCSa7 :		, maked					
	*	800	*	820	*	840	
TrCSa1 :							<b>-</b>
TrCSa2 :							-
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TrCSa5 :	AACTTATGAGGAT	AGCTTGAATTTA	ATTGCTCG'	TTTGCCTGGAA	TIGCIGCCIA	TATTTA:	
TrCSa6 :	AACTTATGAGGATA	AGCTTGAATTTA	ATTGCTCG	I"I"I'GCCTGGAA	TTGCTGCCTA	TATTTA	92
TrCSa7 :	-ACTTATGAGGAT	-GCTTGAATTTA	VAIL.I.GC.I.C.G.	I'I'IGCCIGGAA	TIGCIGCE		
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TrCSa2 :							-
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TrCSa5	TCGACGGATATAC	AAGGATGGAAAA	AATCATACC	ATTGGATGATT	CTTTGGATTI	ATGGTGC	: 531
TrCSa6	TO T	NACCATCCAAA	AATCATACC	'ATTGGATGAT'I	CTTTGGAT 1	AIGGIGC .	493
TrCSa7	TCGACGGATATAC	AAGGATGGAAA	AATCATACC	ATTGGATGATT	CTTTGGATT	ALGGLEC	152
				242		960	
	*	920	*	940			<u> </u>
TrCSa1				·			• • -
TrCSa2							
TrCSa3							: -
TrCSa4	AAACTATGCTCAC	A MORMA CCATT	TCATCATC	TAGAAACGCTG	GAGTTTATGA	GGCTGTA	: 591
TrCSa5	AAACTATGCTCAC	AIGITAGGALL	TGATGATCC	CACALACGCTG	GAGTTTATGA	GGCTGTA	: 553
TrCSa6	AAACTATGCTCAC AAACTATGCTCAC	AIGIIAGGAII ATCTTACCATT	CATCATC	CAGAAACGCTG	GAGTTTATGA	GGCTGTA	: 212
TrCSa7	AAACTATGCTCAC	AIGIIAGOAII	TOMICHIC	31.0.2			
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	*	980	*	1000	*	1020	
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TrCSa3							: <del>-</del>
TrCSa4	:						: 601
TrCSa5	em a concern com a cohi						: 581
TrCSa6		77 CMC 1 MC 1 MC 1	AGGN		CACACACAC	ACCTACT	: 272
TrCSa7		PAGTGATCATGA	AGGIIGGCA.	ACGITIAGITICI	CACACAGCIC	ACCIAGI	. 2,2
	*	1040	*	1060	*	1080	
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TTCSa2							: ~
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TrCSa4	•						: -
TrCSa5 TrCSa6	•						: -
TrCSa6		ATCAGATCCTT	ATCTTGCAT	TCGCAGCTGCT	CTGAATGGTT	TAGCTGG	: 332
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392	TTAAGGA							8a6 :
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	Carloran	ATICATAA	TGAGCGACTAC	CAGAACAAT	AACATAAGTA	AACTCCA	GTTTGG	Sa7 :
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: - : - : - : - : 512					GTGCCTGGA		CAGTG	Sa2 : Sa3 : Sa4 : Sa5 :
: - : - : - : - : 512			GGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	CCAGGT	CAGTGO	Sa2 : Sa3 : Sa4 : Sa5 : Sa6 : Sa7 :
: - : - : - : - : 512			GGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	CCAGGT	CAGTG	Sa2 : Sa3 : Sa4 : Sa5 : Sa6 : Sa7 :
· · · · · · · · · ·			EGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	CCAGGT	CAGTG	Sa2 : Sa3 : Sa4 : Sa5 : Sa6 : Sa6 : Sa7 : Sa1 : Sa2 : Sa3 :
· · · · · · · · · · ·			GGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	CCAGGT	CAGTG	Sa2 : Sa3 : Sa4 : Sa5 : Sa5 : Sa6 : Sa7 : Sa7 : Sa2 : Sa2 : Sa3 :
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· · · · · · · · · ·			GGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	CCAGGT		Sa2 : Sa3 : Sa4 : Sa5 : Sa5 : Sa6 : Sa7 : Sa7 : Sa2 : Sa2 : Sa3 : Sa4 : Sa5 :
· · · · · · · · · · · · · · · · · · ·		AATACAGA	GGAGTTTTGCGC	ATGGACAT	GTGCCTGGA	*		Sa2 : Sa3 : Sa4 : Sa5 : Sa5 : Sa5 : Sa6 : Sa7 : Sa6 : Sa7 : Sa2 : Sa2 : Sa3 : Sa4 :

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maggh .	~NTTTTTTT CNTTT	* r#CC&CAGC	20 ATCCTAATCCT	* AATCCTAA'	40 ICCTAATCCTAT	* TACTAATTA	60 CTA :		60
TrCSb :	CMITICAL	LICCACHOO			•				
TrCSb :	ATTACTAA'	* TTACTAGTA	80 CTAATTAGTAA	* TACCGATC	100 CCTTTTTCTCGA		120 TTC :	1	.20
TrCSb :	AAGNAGAA	* GAAGGAAAA	140 ACAAAATCCAC	* ACAAACAA	160 ACATCTTACAAC		180 CGAC :	1	L80
	a a coma coma	* ~~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	200 	* *CACGACGC	220 TGCACGGAACCO	* ETTTGGCCAC	240 CCT :	2	240
TrCSb :	AACTACTA		MICORIOCIC						•
TrCSb :	CTCAGCTC	* ACTTGCTT	260 CCTTCCTCCACA	* ACCTCCGC	280 CGCGCTCCTCC	* ATCCTATTCA	300 ACCT :	3	300
TrCSb :	ттсттстт	* CCTCCGGG	320 ATCTCCCCACC	* GTCTAATGT	340 CCAAAGGAACAC	* TCACCGTTG	360 FTGA :	;	360
		•	380	*	400 CTCCTGATGGCA	*	420 .		420
TrCSb :	TGAACGIA	ACCGGGAAG.							
TrCSb :	: TGATTTC	* AAGAAGATA	440 TCAACTGGGAA	* GAATGATA	460 AGGGACTCAAAC	* TTTATGATC	480 CTGG :		480
TrCSb	: ATATTTA	* AACACTGCT	500 CCTGTGCGATC	* AACAATTT	520 CTTATATTGATG	* GTGATGAGG	540 GAAT :		540
TrCSb	: CCTTAGA	* TATAGAGGA	560 TACCCCATTGA	* \GGAGTTGG	580 CCGAGAAAAGCA	* \CCTTTCCGG	600 AAGT:	:	600
TrCSb	: GGCATAT	* CTCATATTO	620 TATGGAAATTI	* rgccttcte	640 CAAATCAGTTAC	CAAGAATGGG	060 TTAAE	:	660
TrCSb	: TGCTATA	* TCTCAGCA	680 FTCAGCCTTAC	* CTCAAGGAG	700 STTTTGGATCTC	* ATACAATCAA	720 ATGCC	:	720
TrCSb	: TCAAGAI	* GCACATCC	740 TATGGGCGTCC	* TAGTGAAT(	760 SCAATAAGCGCT	* CTGTCTGTT	780 PTTCA	:	780
TrCSb	: TCCTGAC	* CGCAAATCC	800 TGCTCTCAGAG	* GTCTTGAC	820 ATCTACAACTCA	* AAGCAAGTGI	840 AGAGA	:	840
			860	*	880 ACAATTGCTGCT	w	900		900
TrCSb	: CAAACAI	AATAGCACG		*	940	*	960		
TrCSb	: AATGGC	AGGAAGGCC	920 ACCTGTGCTTC	CATCCAAC	AAACTATCTTAC	ACAGAGAAC	TTCCT	:	960

TrCSb : ATACATGCTTGATTCTCTAGGCAATCGGTCATATAAACCCAACCCTCAGCTAACTCGTGC : 1020 TrCSb : ACTAGACATCATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 1080 TrCSb : ACGACACCTTGCATCAAGCGGCGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 1140 TrCSb : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 1200 \* 1220 TrCsb : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 1244

TrCSb	:	* MSTTTTTTDESKLHDAA	20 RNRLATLSAHLI	* LPSSTTSAJ	40 ALLHPIHLSSSS	* GISPPSNVK	60 CTL	:	60
TrCSb	:	* TVVDERTGKKYTIEVSP	80 DGTVKANDFKK	* ISTGKNDK	GPKPADAGAFNI GPKPADAGAFNI	* 'APVRSTIS'	120 YIDG	:	120
TrCSb	:	* DEGILRYRGYPIEELAE	140 KSTFPEVAYLI	* LYGNLPSA	160 NQLQEWEFAIS(	* OHSALPQGVI	180 LDLI	:	180
TrCSb	:	* QSMPQDAHPMGVLVNAI	200 SALSVFHPDAN	* PALRGLDI	220 Ynskovrdkoli	* ARIIGKITT:	240 IAAA	:	240
TrCSb	:	* INLRMAGRPPVLPSNKI	260 SYTENFLYMLD	* SLGNRSYK	280 PNPQLTRALDI	* IFILHAEHE	300 MINCS	:	300
TrCSb	:	* TSAVRHLASSGVDVYT	JIAGGAGYTAGE 330	* PLHGGANEA	340 AVLKMLSEIGSV	·* DNIPEFIEG	vx :	35	8

egure 104 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSb

	* 20 * 40 <b>*</b> 60	
TrCSb1 :	CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTA	60
TrCSb2 :		-
TrCSb2 :		: -
TrCSb4:		: -
		: -
TrCSb5:		: -
TrCSb6:		: -
TrCSb7 :		
	* 80 * 100 * 120	
	* 80 * 100 ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATT	: 120
TrCSb1 :	ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTTTT	: -
TrCSb2	:	
TrCSb3		· -
TrCSb4	:	
TrCSb5		: -
TrCSb6		
TrCSb7	:	•
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	160 * 180	
		: 179
TrCSb1	: AATTCAAAGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	: 55
TrCSb2		
TrCSb3	CITE CATACA A CCA A A CA CA A A A TRICA CAMACAMA A CATCITA CAACAA I GI CAACCA C	: 58
TrCSb4	TOTAL CONTRACTOR AND MAIOTON A	: 50
TrCSb4		: 45
TrCSb5		: -
		: -
TrCSb7	:	
	* 200 * 220 * 240	
TrCSb1	TO STATE OF A COCCACCA ATTOCA ACCTGCACGACGCTGCACGGAACCGTTTGGCIIACCCT	: 239
TrCSb2	cma cma ca a coca acca a moca a comeca acca comeca	: 115
TrCSb2		: 118
TrCSb4	TO THE CONTROL OF A COCA COA A TOCA A GOTGO A COCACGO I I I AGO COACCO I	: 110
TrCSb5	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGC∏ACCCT	: 105
TrCSb5		: -
TrCSb6		: -
, Trusb/	:	
	* 260 * 280 * 300	
TrCSb1	CTCCACA ANCTOCATCCTTCCTCCACA ANCTCCGCTGCGCTTCCTCCATCCTATCCACCT	: 299
	OMCA COTTO CTTCCTTCCTTCCTCCACACCTCCGCCGCGCTCCTALICACCT	
TrCSb2	COMOR COMOR COMPROMINACION CONTROLLA	
TrCSb3		: 1/0
TrCSb4		: 165
TrCSb5		-
TrCSb6		
TrCSb7	:	
	+ 320 * 340 * 360	
TrCSb1	: TTCTTCTTCTCIJGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA	235
TrCSb2	THE CONTROL OF COCCES AND THE CONTROL AND CONTROL AND CONTROL OF THE CONTROL OF T	
TrCSb3	TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA	: 230
TrCSb4	TTCTTCTTCCTCCCCCATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGIIGIIGA	. 250
TrCSb5	$\sim -22$	. 225
TrCSb6		
TrCSb7		· : -

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		*	380	*	400	*	420	119
TrCSb1	. 1	TGAACGTACCGGG	AAGAAGTATAC	CATTGAGGTC	TCTCCTGATG	GCACCGTTAA	AGCCAA : 4	19 295
TrCSb2				<i>C</i> አጥጥር አርርጥር		JUALLUL LIMP	-10 0 0 -1 - 2	
TrCSb3			* * ~ * * ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	$\sigma$ $\Lambda$ $\sigma$	"I'CACCIGAIG	3CACCGIIAA	-1010 G 2:2	298
TrCSb4			יו איים איים אי איי איי א	A VIII.IA TOTAL COLL	ILLICIOAIO	ししたしししょよここ		290
TrCSb4		TGAACGTACCGGG TGAACGTACCGGG	AAGAAGTATAC	CATTGAGGTC	TCTCCTGATG	GCACCGTTAA	AGCCAA : 2	285
	•	IGAACGIACCGG					:	-
TrCSb6	•						:	-
TrCSb7	:							
		•	440	*	460	*	480	
m-coh1		TGATTTCAAGAAC	A TA TO A A CTGG	GAAGAATGAT	TAAGGGGCTCA	AACTTTATGA	TCCTGG : '	479
TrCSb1	•		マスロスロススス ヘロへん	このカカのみみずにみじ	I'AA(i(i(iACIUA	TAYOTTIME	TCCTCC	355
TrCSb2	•	THE PROPERTY AND	マスカン かんり とんしん	יכא א כי א שרוה א'	<b>PAAGGGACTU</b> A	MACTITATON	recree	358
TrCSb3	•			י תיהות תיה תיהורי	T' A A ( 2 ( 2 ( 2 A ( 2 ) 1 ) ) A	VAALLIIAIOM		350
TrCSb4	:	TGATTTCAAGAAG	ATATOMACTO	GAAGAATGA'	TAAGGGGCTCA	AACTTTATGA	TCCTGG :	345
TrCSb5	:	TGATTTCAAGAAG	MINICANCIO	Office and on			:	-
TrCSb6	:					<u> </u>	:	1
TrCSb7	:				•			
		· · · · · · · · · · · · · · · · · · ·	500	*	520	*	540	
		ATATTTAAACAC	TO CTCCTCTCCC	GATCAACAAT	TTCTTATATTC	SATGGTGATGA	GGGAAT :	539
TrCSb1		3 CO 3 CO CO CO CO	ァベヘͲベヘͲϾͲϾϹ	CATCAACAAT	TTCTTATATT	SAIGGIGALGE		415
TrCSb2		ATATTTAAACAC	racreerarac racreerarac	GATCAACAAT	TTCTTATATT	SATGGTGATG	AGGGAAT :	418
TrCSb3		ATATTTAAACAC	TGCTCCTGTGC	CATCAACAAT	TTCTTATATT	GATGGTGATG	AGGGAAT :	410
TrCSb4		ATATTTAAACAC ATATTTAAACAC	TGCTCCTGTGC	CATCAACAT CATCAACAAT	TTCTTATATT	GATGGTGATG	AGGGAAT :	405
TrCSb5		ATATTTAAACAC	IGCICCIGIGC	GAICAACAAI			:	-
TrCSb6							:	-
TrCSb7	•							
		*	560	*	580	*	. 600	
TrCSb		CCTTAGATATAG	AGGATACCCCA	TTGAAGAGTT	GGCCGAGAAA	AGCACCTTTC	CGGAAGT :	599
TrCSb			<b>カペペカザカペペペペカ</b>	TTCAGGAGT	'GGCCGAGAAA	AGCACCITIC	CCCALCI.	475
TrCSb2		COMMANDA TO TO TO TO TO	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	TTGAGGAGT"	'GGCCGAGAAA	AGCACCTITC	CCCHACA.	478
TrCSb		COMMANDA COMMANDA CO	12 CC 2 TT CCCC 7	$^{\prime}$ TTC $^{\prime}$ CC $^{\prime}$ CT $^{\prime}$	rggccgagaaa	AGCACCTTIC	CGGAAGI	470
TrCSb		CCTTAGATATAG	'A CC A TA CCCCZ	∖™™C¤¤ïG¤G™	reelece e a cara a	AGCACCITIC	CGGMMCI .	465
TrCSb		ATAC	AGGGTCCNA	ATTGAGGAGT:	rgg-cgagaaa	AGCACITTTA	TGGAAGT:	49
TrCSb							:	-
ILCSD	•							
					•			
		*	620	*	640	*	660	600
TrCSb	1	GGCATATCTN					:	609
TrCSb		COOR TO THOMOTOR	DATE CTATECA	AATTTGCCTT	CTGCAAATCAC	STTACAAGAAT	GGGAATT:	535 538
TrCSb		COCA MA MOMOAA	pa がからかみずだに A i		CIGCAAAICAC	TINCHAGNAT	CCCFTTT	
TrCSb		CCCD MD MCMCDCD	ァッサイナン・アンサイト	∆∆ೡೡೡ๘୯୯ೡ۳	CTGCAAATCAG	"I"I'ACAAGAA I	GGGAALI .	530
TrCSb		CONTRACTOR OF CO	armour mocor	ᠵ᠈ᡎᡎᢇᢕᢕᡎᡎ	CTGCAAATCA	J'I"L'ACAAGAA I	GGGAALL	525
TrCSb		PT (TT	ra\text{ATGTATGGA}	agtttäcctä	CTGÄAAĞTAA(	T.T.Y.G.C.T.G.W.T.		108
TrCSb							GGGAATT:	12
11,000	•	•						
							700	
		*	680	*	700	*	720	
TrCSh	1	:				ncmoz mz cz z		589
	_	TGCTATATCTC	AGCATTCAGCC	TTACCTCAAG	GAGTTTTGGA	TCTCATACAA'.	(Vex 8(8)	: 594
		ma ama ma mama	ACCATTCACCC	TTACCTCAAG	GAGTTTTTGGA	TCTCATACAA'		: 570
TrCSb	3	: IGCTATATETE	AGCALICADOC				· ·	
TrCSb TrCSb	3		ゝ┌┌⋋┯┯┌⋋╓┌∁	ΨΤΙΣΙΟΙΟΨΙΚΟΔΙΑΙΟ	(CAVCA 南南南山バー			
	)3 )4	: TGCTATATCTC	AGCATTCAGCC	TTACCTCAAG	GAGTTTTQ= -	TCTCATACAA'	TCAATGCC	: 585
TrCSb	3 4 5	: TGCTATATCTC : TGCTATATCTC	AGCATTCAGCC AGCATTCAGCC	TTACCTCAAC CAACTCAAC	GAGTTTTIGGA GAGTTTTGGA	TCTCATACAA' TÄTCATACAA'	TCAATGCC TCAATGCC	: 585 : 168
TrCSh TrCSh	3 4 5 5 6	: TGCTATATCTC : TGCTATATCTC	AGCATTCAGCC AGCATTCAGCC	TTACCTCAAC CAACTCAAC	GAGTTTTIGGA GAGTTTTGGA	TCTCATACAA' TÄTCATACAA'	TCAATGCC TCAATGCC	: 585

			740	*	760	*	780	
		*	/40				:	-
TrCSb1:							:	-
TrCSb2 :							:	-
TrCSb3 :							:	-
TrCSb4 :	CA A CAINT							592
TrCSb5 :	TCAAGNN	CACATCC'	TATGGGTGTCCT	PAGTGAATG	CAATAAGCGC	TCTHTCTGT:	TTTTCA :	228
TrCSb6 : TrCSb7 :	TCALGAIC	GCACATCC GCACATCC	TATGGGEGTCCT TATGGGCGTECT	TTGTTAATG	CTCTAAGTGC	TTTGTCTGT	rttca :	130
TICSD/:	ICANGAI	ge/ielizoe						
		*	800	*	820	*	840	
TrCSb1 :								_
TrCSb2								-
TrCSb3								_
TrCSb4								_
TrCSb5						CARACCARCT	GAGAGA:	288
TrCSb6	TCCTGAC	GCCAATCC	TGCTCTTAGAG	GTCTTGAU	ATETACGACT	CAAAGGAAGI	GAGAGA:	190
TrCSb7	: TCCTGAT	GCAAATCC	TGCTCTLAGAG	GTCTTGAC.	ATCTACAACI	CAAAGCAAGI	Cincinon	
			0.60	*	880	*	900	
		*	860				:	-
TrCSb1	:						:	-
TrCSb2	:						:	-
TrCSb3							:	-
TrCSb4 TrCSb5	:							-
TrCSb5	0000000	ATTACCAC	CCATTATTGGAZ	ACATHAMA	ACAATTGCTG	CTGCAGTTI	ATCTTAG :	348 250
	• [C./AVAVAVAVAVA		GCALLASSOCIA					
	: CAAACA	AATAGTGC	GGATTATTGGA?	AAGATAACA	ACAATTGCTC	CTGCGATTA!	ATCTTAG:	250
TrCSb7	: CAAACA	AATAGTGC	GGATTAT.IGGAA GGATTATTGGAA	AAGATAACA	ACAATTGCTC	ECTGCĞATTA!	ATCTTAG :	250
	: CAAACAA	AATAGTGC	GGATTATTGGA?	AAGATĀACA	ACAATIGCIC	ectgcgatta <i>i</i>	960	250
TrCSb7	: CAAACAA	AATAGTGC	GGATTATTGGAZ	AGATĀACA	ACAATTGCTG	ectgcßatta) *		-
TrCSb7	: CAAACAA	AATAGTGC	GGATTATTGGA?	AAGATÄÄČÄ *	ACAATIGCIC	*		- -
TrCSb1 TrCSb2	: CAAACAA	AATAGTEC	GGATTATTGGA?	AAGATÄAČA *	ACAATIGCIC	*		
TrCsb1 TrCsb2 TrCsb3	: CAAACAA	*	GGATTATTGGA?	AAGATÄACA *	ACAATIGCIC	*		
TrCsb1 TrCsb2 TrCsb3 TrCsb4	: CAAACA	AATAGIĞC	. 920 .	*	940	*	960	
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5	: CAAACA	AATAGIĞC	. 920 .	*	940	*	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6	: CAAACA	AATAGIĞC	. 920 .	*	940	*	960	
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5	: CAAACA	AATAGIĞC	GGATTATTGGA?	*	940	*	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6	: CAAACA	AATAGIĞC	. 920 .	*	940 940 CAACTATCT	*	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6	: CAAACA	AATAGIĞC	. 920 .	*	940	*	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6	: CAAACA	AATAGIĞC	GGATTATTGGAA 920 920 CACCTGTGCTT	*	940 940 CAACTATCT	*	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7	: CAAACA	* AGGAAGGC AGGAAGGC	920	* CCATCCAAC	940  GAACTATCT CAAACTATCT	* TACACEGAGA TACACAGAGA	960	- - - - - - -
TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7	: CAAACA	* AGGAAGGC AGGAAGGC	920	* CCATCCAAC	940  CAACTATCT CAAACTATCT	* TACACEGAGA TACACAGAGA	960	- - - - - - -
TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7 TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4	: CAAACA	AATAGIĞC	GGATTATTGGAA 920 CACCTGTGCTT CACCTGTTTCTT	* CCATCCAAC	940  GAACTATCT  CAAACTATCT	* TACACIIGAGA TACACAGAGA	960	- - - - 408 310
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb4 TrCsb4 TrCsb5	: CAAACA	* AGGAAGGC AGGAAGGC	920 . 920 . CACCTGTGCTT CACCTGTTTT  980	* CCATCCAAC CCATCCAAC	940  CGAACTATCT CAAACTATCT	* TACACTGAGA TACACAGAGA	960  ACTTCCT  1020	- - - 408 310
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5	: CAAACA	* AGGAAGGC AGGAAGGC	920 . 920 . CACCTGTGCTT CACCTGTTTT  980	* CCATCCAAC CCATCCAAC	940  CGAACTATCT CAAACTATCT	* TACACTGAGA TACACAGAGA	960  ACTTCCT  1020	- - - 408 310
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb4 TrCsb4 TrCsb5	: CAAACA	* AGGAAGGC AGGAAGGC	GGATTATTGGAA 920 CACCTGTGCTT CACCTGTTTCTT	* CCATCCAAC CCATCCAAC	940  CGAACTATCT CAAACTATCT	* TACACTGAGA TACACAGAGA	960  ACTTCCT  1020	- - - 408 310
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5	: CAAACA	* AGGAAGGC AGGAAGGC	GGATTATTGGAA  920  CACCTGTGCTT  CACCTGTÄCTT  980  TCTUTAGGCAAT	* CCATCCAAC CCATCCAAC * * CCGGTCATA	940  CAACTATCT  CAAACTATCT  1000  TAAACCAACTAAACCAACTAAACCAACTAAACCAACTAAACCAACTAACTAAACCAACTAACTAAAACCAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAAACAAAACAAAAACAAAAAA	* TACACTGAGA TACACAGAGA  * CCTCAGCTA	960 ACTTCCT 1020 ACTCGTGC	- - - - 408 310 : - : - : - : 468 : 370
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5	: CAAACA	* AGGAAGGC AGGAAGGC	GGATTATTGGAA  920  CACCTGTGCTT  CACCTGTÄCTT  980  TCTUTAGGCAAT	* CCATCCAAC CCATCCAAC * * CCGGTCATA	940  CAACTATCT  CAAACTATCT  1000  TAAACCAACTAAACCAACTAAACCAACTAAACCAACTAAACCAACTAACTAAACCAACTAACTAAAACCAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAACTAAAACCAAAACAAAACAAAAACAAAAAA	* TACACTGAGA TACACAGAGA  * CCTCAGCTA	960 ACTTCCT 1020 ACTCGTGC	- - - - 408 310 : - : - : - : 468 : 370
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb5	: CAAACA	AATAGIĞC  * AGGAAGGC AGGAAGGC * TGCTTGAT	920 CACCTGTGCTT CACCTGTÄCTT  980  ICTÜTAGGCAAT	* CCATCCAAC CCATCCAAC  * CGGTCATA	940  CEAACTATCT CAAACTHTCT  1000  TAAACCCAACTAAACCHAA	* TACACTGAGA TACACAGAGA  * CCTCAGCTAF	960 ACTTCCT 1020 ACTCGTGC ACTCGTGC	- - - 408 310 : - : - : - : 468 : 370
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb5 TrCsb6 TrCsb7	: CAAACA	AATAGIEC  * AGGAAGGC AGGAAGGC  * TGCTTGAT	920  CACCTGTGCTT CACCTGTTT  980  CTTTTAGGCAAT  CTCTTTGGCAAT	* CCATCCAAC CCATCCAAC * * CCGGTCATA	940  EGAACTATCT  CAAACTATCT  1000  TAAACCCAACTAAACCTAAA	* TACACTGAGA TACACAGAGA  * CCTCAGCTA	960 ACTTCCT 1020 ACTCGTGC ACTCGTGC	- - - 408 310 : - : - : - : 468 : 370
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb5	: CAAACA	AATAGIEC  * AGGAAGGC AGGAAGGC * TGCTTGAT	920  CACCTGTGCTT CACCTGTÄCTT 980  TCTUTAGGCAAT TCTCTÜGGCAAT	* CCATCCAAC CCATCCAAC * * CCGGTCATA	940  CAACTATCT  CAAACTATCT  1000  TAAACCCAACTAAACCTAAACCTAAACCTAAACCTAAACCTAACTAACCTAACTAACCTAACTAACTAAACCTAACTAACTAAACCTAACTAAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACTAACTAACCTAACTAAACCTAACTAACTAACTAACCTAACTAACTAACCTAACTAACTAACCTAAACCTAAC	* TACACTGAGA TACACAGAGA  * CCTCAGCTA	960 ACTTCCT 1020 ACTCGTGC ACTCGTGC	
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb6 TrCsb7	: CAAACA	AATAGIEC  * AGGAAGGC AGGAAGGC * TGCTTGAT	920  CACCTGTGCTT  CACCTGTTCTT  980  CTTTTAGGCAAT  CTCTTTGGCAAT	* CCATCCAAC CCATCCAAC * * CCGGTCATA	940  CAACTATCT  AAACTATCT  1000  TAAACCAACTAAACCAACTAAACCAACTAAACCAACTAAACCAACTAACCAACTAAACCAACTAAACCAACTAAAACCAACAA	* TACACEGAGA TACACAGAGA  * CCTCAGCTAA	960 ACTTCT 1020 ACTCGTGC ACTCGTGC	
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb5 TrCsb6 TrCsb7	: CAAACA	AATAGIEC  * AGGAAGGC AGGAAGGC * * TGCTTGAT	GGATTATTGGAA  920  CACCTGTGCTT  CACCTGTTTT  980  TCTTTAGGCAAT TCTCTTTGGCAAT	* CCATCCAAC CCATCCAAC * * * * * * * * * * * * * * * * *	940  CAACTATCT  CAAACTATCT  1000  TAAACCCAACTAAACCTAAACCTAAACCTAAACCTAAACCTAACTAACCTAACTAACCTAACTAACTAAACCTAACTAACTAAACCTAACTAAACCTAACTAAACCTAACTAAACCTAACTAAACCTAACTAAACCTAACTAAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACTAACCTAACTAAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACTAACCTAACTAACTAACCTAACTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACTAACCTAACTAACTAACCTAACTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACCTAACTAACTAACCTAACTAACTAACTAACTAACTAACTAACCTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACAAC	* TACACTGAGA TACACAGAGA  * CCTCAGCTA	960 ACTTCCT 1020 ACTCGTGC ACTCGTGC	
TrCsb7  TrCsb1 TrCsb3 TrCsb4 TrCsb5 TrCsb6 TrCsb7  TrCsb1 TrCsb2 TrCsb3 TrCsb4 TrCsb5 TrCsb4 TrCsb5 TrCsb5 TrCsb5 TrCsb5 TrCsb5 TrCsb6 TrCsb7	: CAAACA	AATAGIEC  * AGGAAGGC AGGAAGGC  * TGCTTGAT	920  CACCTGTGCTT  CACCTGTTCTT  980  CTTTTAGGCAAT  CTCTTTGGCAAT	* CCATCCAAC CCATCCAAC * CCGGTCATA CCGGTCATA	940  CAACTATCT  CAACTATCT  1000  TAAACCCAACTAAACCTAAACCTAAACCTAAACCTAAACCTAAACCTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAACCTAAATTAAAA	* TACACIGAGA TACACAGAGA  * CCTCAGCTAF CCTCGTCTAF	960 ACTTCCT 1020 ACTCGTGC ACTCGTGC 1080	

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			•	1100	*	1120	*	1140	
				1100				:	-
TrCSb1	:							:	-
TrCSb2 TrCSb3	:							:	-
TrCSb3	:							:	-
TrCSb4								:	
TrCSb5		CCGACAC	CTTGCA'	TCAAGCGGCGT	GATGTATA[	ACTGCTATT	GCTGGGGN		579
TrCSb7	•	ACGCCAC	CTTGCA'	TCAAGCGGCGT TCAAG∏GG∏GT	CGATGTATAC	ACTGCTATT	GCTGGAGGTGT	TGGAGC:	490
		7		, , , , , , , , , , , , , , , , , , , ,					
							*	1200	
			*	1160	*	1180	*	1200	_
TrCSb1	:								_
TrCSb2	:								_
TrCSb3	:								-
TrCSb4	:								-
TrCSb5	:								
TrCSb6	:			CTTCATGGTGG	ACCTA ATCA	GCGGTCCTT	AAAATGCTGA	GTGAAAT	: 550
TrCSb7	:	TCTGTAT	'GGACC'I	CTTCATGGIGG	AGCIAAIOA	30000100			
			*	1220	*	.1240			
TrCSb1							- : -		
TrCSb2							- : -		
TrCSb3							·- : -		
TrCSb4							: -		
TrCSb5	:						· <b>-</b> : -		
TrCSb6	:								
TrCSb7	:	TGGAAG	TGTCGA:	TAACATTCCAG	AGTTCATTGA	AGGTGTTAAL	110 : 594		
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